



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 121370

To: Sarvamangala Devi
Location: REM 3C18
Art Unit: 1645
Thursday, May 06, 2004

Case Serial Number: 09/878781

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Shears, Beverly

From: Devi, Sarvamangala
Sent: Wednesday, May 05, 2004 11:12 AM.
To: Shears, Beverly
Subject: 09/878,781

Good morning Beverly:

Please perform a sequence and an interference search for SEQ ID NO: 4 in application SN 09/878,781.

Thanks.

S. DEVI, Ph.D.
AU 1645
Rems - 3C18



STAFF USE ONLY

Date completed: ~~05~~ 05-06-04
Searcher: Beverly c 2528
Terminal time: 23
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

____ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other CGN

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:15:43 ; Search time 45 Seconds
(without alignments)
2355.869 Million cell updates/sec

Title: US-09-878-781-4

Perfect score: 1715
Sequence: 1 MVKVGVNGFGRIGRLAFRR.....EMSTYQVRLTLEPAKIAK 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_nbc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_ricent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1715	100.0	336	2	Q83ZF7 streptococc
2	1618	94.3	336	2	Q8KVU6 streptococc
3	1609	93.8	336	2	Q9ALW2 streptococc
4	1609	93.8	336	16	Q8E3B8 streptococc
5	1609	93.8	336	16	Q8DXS8 streptococc
6	1596	93.1	336	2	Q8GCR7 streptococc
7	1593.5	92.9	335	16	Q97NLI streptococc
8	1593.5	92.9	359	16	Q8CWN6 streptococc
9	1584	92.4	336	2	Q8KHG1 streptococc
10	1579.5	92.1	337	16	Q8DVT3 streptococc
11	1578	92.0	336	2	Q8KVU5 streptococc
12	1572	91.7	336	2	Q8VVB9 streptococc
13	1518	88.5	320	2	Q9L5X6 streptococc
14	1468.5	85.6	309	2	Q9AUT7 streptococc
15	1467.5	85.6	309	2	Q9AUT9 streptococc
16	1465.5	85.5	309	2	Q9AUT4 streptococc

17	1463.5	85.3	309	2	Q9AUT5 streptococc
18	1462.5	85.3	308	2	Q9AUT8 streptococc
19	1445.5	84.3	305	2	Q9AUT6 streptococc
20	1410	82.2	336	16	Q9CDH4 streptococc
21	1337.5	78.0	333	16	Q83318 streptococc
22	1262	73.6	336	16	Q8V411 streptococc
23	1261	73.5	336	16	Q928H9 streptococc
24	1227.5	71.6	332	16	Q8XKT9 streptococc
25	1218.5	71.0	335	16	Q8RFP9 streptococc
26	1197.5	69.8	334	16	Q9VWT8 streptococc
27	1190	69.4	336	16	Q8CPY5 streptococc
28	1189.5	69.4	330	2	Q833X3 streptococc
29	1186.5	69.2	330	2	Q84HZ6 streptococc
30	1185.5	69.1	330	2	Q84HZ4 streptococc
31	1184.5	69.1	334	16	Q9VX95 streptococc
32	1183	69.0	336	16	Q9ZSC5 streptococc
33	1182.5	69.0	330	2	Q84HZ5 streptococc
34	1178.5	68.7	335	2	Q93M61 streptococc
35	1138	66.4	311	2	Q8L2R0 streptococc
36	1132.5	66.0	310	2	Q8L2P7 streptococc
37	1124.5	65.6	310	2	Q8L2P6 streptococc
38	1124	65.5	311	2	Q8L2P8 streptococc
39	1123.5	65.5	310	2	Q8L2O6 streptococc
40	1121.5	65.4	311	2	Q8VW79 streptococc
41	1120.5	65.3	310	2	Q8L2O3 streptococc
42	1120.5	65.3	310	2	Q8L2P5 streptococc
43	1118.5	65.2	310	2	Q8L2Q2 streptococc
44	1116.5	65.1	310	2	Q8L2R7 streptococc
45	1115.5	65.0	310	2	Q8L2R2 streptococc

ALIGNMENTS

RESULT 1
Q83ZF7 PRELIMINARY; PRT; 336 AA.

AC Q83ZF7; TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glyceraldehyde 3-P dehydrogenase.
GN GAPC.
OS Streptococcus dysgalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1334;
RN [1]
RP SEQUENCE FROM N.A.
RA Peres-Casal J.F., Bolton A., Song X.-M., Willson P., Potter A.A.:
RT "Use of the surface proteins gaps and Mlg of Streptococcus
RT dysgalactiae as protective antigens against mastitis in non-lactating
RT cows";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF375662; AAP31408.1; -
DR GO; GO:0004365; P:glyceraldehyde-3-phosphate dehydrogenase (p...); IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR006424; GAPDH-1.
DR InterPro; IPR000173; GAP_dhhydrogenase.
DR Pfam; PF00044; gpdh.1.
DR Pfam; PF02800; gpdh_C.1.
DR PRINTS; PR00078; G3PDHGNASE.
DR TIGRFAMs; TIGR01534; GAPDH-I.1.
DR PROSITE; PS00071; GAPDH; 1.
SQ SEQUENCE 336 AA; 35928 MW; 11828218CF037076 CRC64;

Query Match 100.0%; Score 1715; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.7e-107;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVKVGNGFGRIGRLAFRRIONVGVETVRINDLDPVMAHLIKYDTQGRFDIVAV 60
DB 1 MVKVGNGFGRIGRLAFRRIONVGVETVRINDLDPVMAHLIKYDTQGRFDIVAV 60

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QY 61 KEGGEVNGNFIVKSAERDENIDMATDGVETIUBATGPACKEAENHANGAKKVI 120
DB 61 KEGGEVNGNFIVKSAERDENIDMATDGVETIUBATGPACKEAENHANGAKKVI 120
QY 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180
DB 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180
QY 181 YTGDMQMLDGPBHGDLRRARAGANIVPNSGAAKAIIGVIPLENGKLDGAAGRPVPT 240
DB 181 YTGDMQMLDGPBHGDLRRARAGANIVPNSGAAKAIIGVIPLENGKLDGAAGRPVPT 240
QY 241 GSVTELVVTLDKNVSVDENINAMKAASNDSPGTEPDIYSSDIYVSGSLFPAATQTKVM 300
DB 241 GSVTELVVTLDKNVSVDENINAMKAASNDSPGTEPDIYSSDIYVSGSLFPAATQTKVM 300
QY 301 EVDGSOQVKNVSVNEMSYTAOLVTLTEYFAKIK 336
DB 301 EVDGSOQVKNVSVNEMSYTAOLVTLTEYFAKIK 336

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RESULT 2

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Q8KV06 PRELIMINARY; PRT: 336 AA.
ID Q8KV06
AC Q8KV06;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase.
OS Streptococcus uberis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
NCBI_TaxID=1349;
XN [1]
XP SEQUENCE FROM N.A.
RA STRAIN=ATCC 9927;
RA Fontaine M.C., Perez-Casal J., Song X.-M., Sheldford J., Willson P.J.,
RA Potter A.A.;
RT "Immunitation of dairy cattle with recombinant GapC and chimeric CAMP
RT streptococcus uberis.";
RT antiserum confers protection against heterologous challenge with
RT Streptococcus uberis.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.
EMBL: AF421390; AAM7371.1;
DR GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR006424; GAPDH-I.
DR InterPro: IPR000173; GAP_dhdtrogenase.
DR Pfam: PF00044; spdh. 1.
DR Pfam: PF02800; GAPDH-I.
DR PRINTS: PR00078; G3BDHGNAS.
DR TIGRfam: TIGR01534; GAPDH-I. 1.
DR PROSITE: PS00071; GAPDH; 1.
KW Oxidoreductase.
SQ SEQUENCE 336 AA; 35906 MW; 755D7A4548E61D4 CRC64;

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Query Match 94.3%; Score 1618; DB 2; Length 336;
 Best Local Similarity 92.9%; Pred. No. 1.8e-100;
 Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MVAKVGINGFGIGRLAFRIQVNGEVETRIINDLTPNMLAHILKYDTTQGRPDGVET 60
DB 1 MVAKVGINGFGIGRLAFRIQVNGEVETRIINDLTPNMLAHILKYDTTQGRPDGVET 60
QY 61 KEGGEVNGNFIVKSAERDENIDMATDGVETIUBATGPACKEAENHANGAKKVI 120
DB 61 KEGGEVNGNFIVKSAERDENIDMATDGVETIUBATGPACKEAENHANGAKKVI 120
QY 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180
DB 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180

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DB 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180
QY 181 YTGDMQMLDGPBHGDLRRARAGANIVPNSGAAKAIIGVIPLENGKLDGAAGRPVPT 240
DB 181 YTGDMQMLDGPBHGDLRRARAGANIVPNSGAAKAIIGVIPLENGKLDGAAGRPVPT 240
QY 241 GSVTELVVTLDKNVSVDENINAMKAASNDSPGTEPDIYSSDIYVSGSLFPAATQTKVM 300
DB 241 GSVTELVVTLDKNVSVDENINAMKAASNDSPGTEPDIYSSDIYVSGSLFPAATQTKVM 300
QY 301 EVDGSOQVKNVSVNEMSYTAOLVTLTEYFAKIK 336
DB 301 EVDGSOQVKNVSVNEMSYTAOLVTLTEYFAKIK 336

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RESULT 3

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Q9ALM2 PRELIMINARY; PRT: 336 AA.
ID Q9ALM2
AC Q9ALM2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
NCBI_TaxID=1311;
XN [1]
XP SEQUENCE FROM N.A.
RA STRAIN=J48;
RA Selfert K.N., Blaisais A.S., McArthur W.P., Brady L.J.;
RT "The Group B Streptococcal Surface Antigen Delta is a Glyceraldehyde
RT 3-Phosphate Dehydrogenase.";
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.
EMBL: AF338416; AAK14387.1;
DR HSP: P00362; IGDI.
DR GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR006424; GAPDH-I.
DR InterPro: IPR000173; GAP_dhdtrogenase.
DR Pfam: PF00044; spdh. 1.
DR Pfam: PF02800; GAPDH-I.
DR PRINTS: PR00078; G3BDHGNAS.
DR TIGRfam: TIGR01534; GAPDH-I. 1.
DR PROSITE: PS00071; GAPDH; 1.
KW Oxidoreductase.
SQ SEQUENCE 336 AA; 36005 MW; 982EL8K05CA343C9 CRC64;

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Query Match 93.8%; Score 1609; DB 2; Length 336;
 Best Local Similarity 92.0%; Pred. No. 7.2e-100;
 Matches 309; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MVAKVGINGFGIGRLAFRIQVNGEVETRIINDLTPNMLAHILKYDTTQGRPDGVET 60
DB 1 MVAKVGINGFGIGRLAFRIQVNGEVETRIINDLTPNMLAHILKYDTTQGRPDGVET 60
QY 61 KEGGEVNGFIVKSAERDENIDMATDGVETIUBATGPACKEAENHANGAKKVI 120
DB 61 KEGGEVNGFIVKSAERDENIDMATDGVETIUBATGPACKEAENHANGAKKVI 120
QY 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180
DB 121 TAPGNDVKTIVNTNHDILDTGTVISGASCTTNCIAPMAKALDPAFGIOGLMTTIIA 180
QY 181 YTGDMQMLDGPBHGDLRRARAGANIVPNSGAAKAIIGVIPLENGKLDGAAGRPVPT 240
DB 181 YTGDMQMLDGPBHGDLRRARAGANIVPNSGAAKAIIGVIPLENGKLDGAAGRPVPT 240
QY 241 GSVTELVVTLDKNVSVDENINAMKAASNDSPGTEPDIYSSDIYVSGSLFPAATQTKVM 300
DB 241 GSVTELVVTLDKNVSVDENINAMKAASNDSPGTEPDIYSSDIYVSGSLFPAATQTKVM 300

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Db 241 GSVTELVATLEKDVTEVEVNAAMKAANDSYGTEDPYVSSDIIWJISYSLFPAOTQKVQ 300
QY 301 EVDGSQLVYVSWYNDENMSYTAQVLTLEFPKIAK 336
Db 302 TVDGNQLVKVVSWYNDENMSYTSQVLTLEFPKIAK 336

RESULT 4

Q8E3E8 PRELIMINARY; PRT: 336 AA.

AC Q8E3E8; 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase.
GN G8S1811.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM516 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Ruenliok C., Buchliesser C., Chevalier F., Frangoul L.,
RA Masdek T., Zouine M., Couve E., Talhouk L., Poyart C., Trieu-Quot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1511(2002).
DR EMBL; AL766853; CAD47470.1; -.
DR GO; GO:0053365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR006424; GAPDH-I.
DR InterPro; IPR000173; GAP_dhrogenase.
DR Pfam; PF00044; gpdh.1.
DR Pfam; PF02800; gpdh.C.1.
DR PRINTS; PR00078; G3PDHDSGNASE.
DR TIGRPFAM; TIGR01534; GAPDH-1; 1.
DR PROSITE; PS00071; GAPDH; 1.
KM Complete proteome.
SQ SEQUENCE 336 AA; 36005 MW; 982E18A05CA343C9 CRC64;

Query Match 93.8%; Score 1609; DB 16; Length 336;
Best Local Similarity 92.0%; Pred. No. 7.2e-100;
Matches 309; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 1 MVTYVINGEGRIGR-LAFRIQNVGEVTRINDLTPMMLAHLLKXDTTQGRFGTVEV 60
Db 1 MVTYVINGEGRIGR-LAFRIQNVGEVTRINDLTPMMLAHLLKXDTTQGRFGTVEV 60
QY 61 KEGGEFVNGFPIKVAERDPENIDMATGVEIVLEATGFPACKAEKHLHANGAKKVI 120
Db 61 KEGGEFVNGFPIKVAERDPENIDMATGVEIVLEATGFPACKAEKHLHANGAKKVI 120
QY 121 TAPGANDVKTVPNNHNDLIDGTEIVISGASCTNCLAPMAKALDPAFGIOKGLMTTIIA 180
Db 121 TAPGANDVKTVPNNHNDLIDGTEIVISGASCTNCLAPMAKALDPAFGIOKGLMTTIIA 180
QY 181 YTGDMILDPHRRGDLRRARAGANIVPNSGAAGAIGLVIPELNGKLDGAAGRVPT 240
Db 181 YTGDMILDPHRRGDLRRARAGANIVPNSGAAGAIGLVIPELNGKLDGAAGRVPT 240
QY 241 GSVTELVATLEKDVTEVEVNAAMKAANDSYGTEDPYVSSDIIWJISYSLFPAOTQKVQ 300
Db 241 GSVTELVATLEKDVTEVEVNAAMKAANDSYGTEDPYVSSDIIWJISYSLFPAOTQKVQ 300
QY 301 EVDGSQLVYVSWYNDENMSYTAQVLTLEFPKIAK 336
Db 301 TVDGNQLVKVVSWYNDENMSYTSQVLTLEFPKIAK 336

RESULT 5

Q8DXS8 PRELIMINARY; PRT: 336 AA.

AC Q8DXS8; 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase.
GN GAP OR SAG1768.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettein H., Masiqani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Messels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beaman M.J., Brinkac R., Daugherty S.C.,
RA Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Kouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarcelli M., Mora M.,
RA Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegen F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014272; AAN00631.1; -.
DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR006424; GAPDH-I.
DR InterPro; IPR000173; GAP_dhrogenase.
DR Pfam; PF00044; gpdh.1.
DR Pfam; PF02800; gpdh.C.1.
DR PRINTS; PR00078; G3PDHDSGNASE.
DR TIGRPFAM; TIGR01534; GAPDH-1; 1.
DR PROSITE; PS00071; GAPDH; 1.
KM Complete proteome.
SQ SEQUENCE 336 AA; 36005 MW; 982E18A05CA343C9 CRC64;

Query Match 93.8%; Score 1609; DB 16; Length 336;
Best Local Similarity 92.0%; Pred. No. 7.2e-100;
Matches 309; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 1 MVTYVINGEGRIGR-LAFRIQNVGEVTRINDLTPMMLAHLLKXDTTQGRFGTVEV 60
Db 1 MVTYVINGEGRIGR-LAFRIQNVGEVTRINDLTPMMLAHLLKXDTTQGRFGTVEV 60
QY 61 KEGGEFVNGFPIKVAERDPENIDMATGVEIVLEATGFPACKAEKHLHANGAKKVI 120
Db 61 KEGGEFVNGFPIKVAERDPENIDMATGVEIVLEATGFPACKAEKHLHANGAKKVI 120
QY 121 TAPGANDVKTVPNNHNDLIDGTEIVISGASCTNCLAPMAKALDPAFGIOKGLMTTIIA 180
Db 121 TAPGANDVKTVPNNHNDLIDGTEIVISGASCTNCLAPMAKALDPAFGIOKGLMTTIIA 180
QY 181 YTGDMILDPHRRGDLRRARAGANIVPNSGAAGAIGLVIPELNGKLDGAAGRVPT 240
Db 181 YTGDMILDPHRRGDLRRARAGANIVPNSGAAGAIGLVIPELNGKLDGAAGRVPT 240
QY 241 GSVTELVATLEKDVTEVEVNAAMKAANDSYGTEDPYVSSDIIWJISYSLFPAOTQKVQ 300
Db 241 GSVTELVATLEKDVTEVEVNAAMKAANDSYGTEDPYVSSDIIWJISYSLFPAOTQKVQ 300
QY 301 EVDGSQLVYVSWYNDENMSYTAQVLTLEFPKIAK 336
Db 301 TVDGNQLVKVVSWYNDENMSYTSQVLTLEFPKIAK 336

RESULT 6

Q8GCR7 PRELIMINARY; PRT; 336 AA.

AC Q8GCR7; 01-VAR-2003 (TREMblrel, 23, Created)

DT 01-VAR-2003 (TREMblrel, 23, Last sequence update)

DT 01-VAR-2003 (TREMblrel, 23, Last sequence update)

DT 01-OCT-2003 (TREMblrel, 25, Last annotation update)

DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).

OS Streptococcus suis.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

NCBI_TaxID=1307;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=5735;

RA Brassard U., Gottschalk M., Quesy S.;

RT Cloning and purification of Streptococcus suis serotype 2

RT glyceralddehyde-3-phosphate dehydrogenase.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY167026; AAB6058.1; -

DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006096; P:glycolysis; IEA.

DR InterPro; IPR006424; GAPDH-I.

DR InterPro; IPR000173; GAP_dhydrogenase.

DR Pfam; PF00044; gpdh; 1. _dhydrogenase.

DR Pfam; PF02800; gpdh; 1.

DR PRINTS; PR00078; G3PDHDMASE.

DR TIGRFAMs; TIGR01534; GAPDH-I; 1.

DR PROSITE; PS00071; GAPDH; 1.

KW Oxidoreductase.

SEQUENCE 336 AA; 35825 MW; 1DBB9B1A492DF59 CRC64;

Query Match 93.1%; Score 1596; DB 2; Length 336;

Best Local Similarity 91.1%; Pred. No. 5,4e-99;

Matches 306; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

QY 1 M V V K G I N G F R I G R I A F R I O N V E G V T R I N D L T D P N M L A H L K T D T O G R P D G T V E V 60

DB 1 M V V K G I N G F R I G R I A F R I O N V E G V T R I N D L T D P N M L A H L K T D T O G R P D G T V E V 60

QY 61 K E G G E V N G N F I K V S A R D P E N I M A T D G V E I V L E A T G F P A K K E A A R K H L A N G A K K V I 120

DB 61 K E G G E V N G N F I K V S A R D P E N I M A T D G V E I V L E A T G F P A K K E A A R K H L A N G A K K V I 120

QY 121 T A P G N D V K T V E N T N H D I L D G T E V I S G A S C T T N C L A P M A K A L H D A F I O G M T T I H A 180

DB 121 T A P G N D V K T V E N T N H D I L D G T E V I S G A S C T T N C L A P M A K A L H D A F I O G M T T I H A 180

QY 181 Y T G D Q M I L D G P H R G C D L R R A P A G A N I V P N S T G A A K A I G V I P E I N G K L D G A A Q R V P P T 240

DB 181 Y T G D Q M I L D G P H R G C D L R R A P A G A N I V P N S T G A A K A I G V I P E I N G K L D G A A Q R V P P T 240

QY 241 G S V T E L V T L D K N V S V D E I N A A K A A S N D S F G T E D P I V S S D I V G S Y G S L F D A T O T K M 300

DB 241 G S V T E L V T L D K N V S V D E I N A A K A A S N D S F G T E D P I V S S D I V G S Y G S L F D A T O T K M 300

QY 301 E V D S G Q L V K V S M Y N D N E S Y T A Q L V T L E Y F A K I A K 336

DB 301 E V D S G Q L V K V S M Y N D N E S Y T A Q L V T L E Y F A K I A K 336

DB 301 E V D S G Q L V K V S M Y N D N E S Y T A Q L V T L E Y F A K I A K 336

RESULT 7

Q97NLI PRELIMINARY; PRT; 335 AA.

AC Q97NLI; 01-VAR-2001 (TREMblrel, 18, Created)

DT 01-VAR-2001 (TREMblrel, 18, Last sequence update)

DT 01-VAR-2001 (TREMblrel, 18, Last sequence update)

DT 01-OCT-2003 (TREMblrel, 25, Last annotation update)

DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC BAA-334 / TIGR4;

RA MEDLINE=21357209; PubMed=11463916;

RA Tettelin H., Nelson K.B., Paulsen I.T., Eisen J.A., Read T.D.,

RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,

RA Durkin A.S., Gwin M., Kolonay J.F., Nelson W.C., Peterson J.D.,

RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

RA Holtzaple B., Knouri H., Wolf A.M., Uterback T.R., Hansen C.L.,

RA McDonald L.A., Feldblyum T.V., Anguilo S., Dickson T., Hickey E.K.,

RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

RT "Complete genome sequence of a virulent isolate of Streptococcus

RT pneumoniae";

RL Science 293:498-506(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC11733;

RA Bergmann S., Hammer Schmidt S.;

RT Identification of pneumococcal GAPDH as plasmin(ogen)-binding

RT protein.;" (Aug-2002) to the EMBL/GenBank/DBJ databases.

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE007490; AK76079.1; -

DR EMBL; AJ058822; CAD44376.1; -

DR PIR; P95235; P95235.

DR HSP; P00354; 3GPD.

DR TIGR; SP0012; -

DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.

DR GO; GO:0006096; P:glycolysis; IEA.

DR InterPro; IPR006424; GAPDH-I.

DR InterPro; IPR000173; GAP_dhydrogenase.

DR Pfam; PF00044; gpdh; 1.

DR Pfam; PF02800; gpdh; 1.

DR PRINTS; PR00078; G3PDHDMASE.

DR TIGRFAMs; TIGR01534; GAPDH-I; 1.

DR PROSITE; PS00071; GAPDH; 1.

KW Oxidoreductase; Complete proteome.

SEQUENCE 335 AA; 35856 MW; DA483CEA423E747B CRC64;

Query Match 92.9%; Score 1593.5; DB 16; Length 335;

Best Local Similarity 92.6%; Pred. No. 7.9e-99;

Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 M V V K G I N G F R I G R I A F R I O N V E G V T R I N D L T D P N M L A H L K T D T O G R P D G T V E V 60

DB 1 M V V K G I N G F R I G R I A F R I O N V E G V T R I N D L T D P N M L A H L K T D T O G R P D G T V E V 60

QY 61 K E G G E V N G N F I K V S A R D P E N I M A T D G V E I V L E A T G F P A K K E A A R K H L A N G A K K V I 120

DB 61 K E G G E V N G N F I K V S A R D P E N I M A T D G V E I V L E A T G F P A K K E A A R K H L A N G A K K V I 120

QY 121 T A P G N D V K T V E N T N H D I L D G T E V I S G A S C T T N C L A P M A K A L H D A F I O G M T T I H A 180

DB 121 T A P G N D V K T V E N T N H D I L D G T E V I S G A S C T T N C L A P M A K A L H D A F I O G M T T I H A 180

QY 181 Y T G D Q M I L D G P H R G C D L R R A P A G A N I V P N S T G A A K A I G V I P E I N G K L D G A A Q R V P P T 240

DB 181 Y T G D Q M I L D G P H R G C D L R R A P A G A N I V P N S T G A A K A I G V I P E I N G K L D G A A Q R V P P T 240

QY 241 G S V T E L V T L D K N V S V D E I N A A K A A S N D S F G T E D P I V S S D I V G S Y G S L F D A T O T K M 300

DB 241 G S V T E L V T L D K N V S V D E I N A A K A A S N D S F G T E D P I V S S D I V G S Y G S L F D A T O T K M 300

QY 300 D V D S G Q L V K V S M Y N D N E S Y T A Q L V T L E Y F A K I A K 335

DB 300 D V D S G Q L V K V S M Y N D N E S Y T A Q L V T L E Y F A K I A K 335

RESULT 8

Q8CNR6 PRELIMINARY; PRT; 359 AA.

AC Q8CNR6; 01-VAR-2001 (TREMblrel, 18, Created)

DT 01-VAR-2001 (TREMblrel, 18, Last sequence update)

DT 01-VAR-2001 (TREMblrel, 18, Last sequence update)

DT 01-OCT-2003 (TREMblrel, 25, Last annotation update)

DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

01-MAR-2003 (TrEMBLrel. 23, Created)
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Glyceraldehyde 3-phosphate dehydrogenase [phosphorylating]
 (EC 1.2.1.12)
 GAPD OR SPR1825.
 Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 NCBI_TaxID=171101;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=21429245; PubMed=11544234;
 Hoskins J., Albom W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
 Dehoff B.S., Estren S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
 Gilmore R., Glass J.S., Klotz H., Kraft A.R., Lagace R.E.,
 LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
 McHaren S.M., McHenry M., Mcleaster K., Mundy C.W., Nicas T.I.,
 Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
 Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
 Zook C.A., Baltz R.H., Taskunas S.R., Rostock P.R. Jr., Skarnd P.L.,
 Glas J.I.,
 "Genome of the bacterium Streptococcus pneumoniae strain R6."
 J. Bacteriol. 183:5709-5717(2001).
 EMBL: A3008547; AAL00628.1; -
 PIR: G98099; G98099.
 GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IEA.
 GO: GO:0016491; F:oxidoreductase activity; IEA.
 GO: GO:0006096; P:glycolysis; IEA.
 InterPro: IPR006424; GAPDH-1.
 InterPro: IPR00173; GAP_dhdrogenase.
 Pfam: PF02800; gpdh. C. 1.
 PRINTS: PR00078; G3PDHGNASE.
 TIGRFAMs: TIGR01534; GAPDH-1; 1.
 PROSITE: PS00071; GAPDH. 1.
 Oxidoreductase; Complete proteome.
 SEQUENCE 359 AA; 38763 MW; 61EF0E35B30860 CRC64;

Query Match 92.9%; Score 1593.5; DB 16; Length 359;
 Best Local Similarity 92.6%; Pred. No. 8.7e-99;
 Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

1 M V V K G I N G F R I G R I A F R I O N V G E V T R I N D L T D P M L A H L K Y D T T G R F D G T V E V 60
 25 M V V K V I N G F R I G R I A F R I O N V G E V T R I N D L T D P M L A H L K Y D T T G R F D G T V E V 84
 61 K E G F E V N G F I K V S A R D E P N I M A T D G V E I V L E A T G F P A K K A A E K H L H A N G A K K V I 120
 85 K E G F E V N G F I K V S A R D E P Q I D M A T D G V E I V L E A T G F P A K K A A E K H L K G A K K V I 143
 121 T A P G S N D V K V V N T N H D I L D G T E V I S G A S C T T N C L A P M A K L H D A F G I O K G I M T T H A 180
 144 T A P G S N D V K V V N T N H D I L D G T E V I S G A S C T T N C L A P M A K L H D A F G I O K G I M T T H A 203
 181 Y T G D Q M I L D G P H R G D L R R A R A G A N I V P N S T G A A K A I G L V I P E I N G K L D G A A Q R V P V P T 240
 204 Y T G D Q M I L D G P H R G D L R R A R A G A N I V P N S T G A A K A I G L V I P E I N G K L D G A A Q R V P V P T 263
 241 G S V T E L V A V L E K T S V E E I N A M A K A A N D S F G T E D P I V S S D I V G S G L F D A T Q T K V 300
 264 G S V T E L V A V L E K T S V E E I N A M A K A A N D S F G T E D P I V S S D I V G S G L F D A T Q T K V 323
 301 E V D S Q L V K V S W D N E M S Y T A Q L V R T L E F A K I A K 336
 324 D V D K Q L V K V S W D N E M S Y T A Q L V R T L E F A K I A K 359

RESULT 9
 08KHG1 PRELIMINARY; PRT; 336 AA.
 08KHG1
 AC 01-OCT-2002 (TrEMBLrel. 22, Created)

01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Glyceraldehyde-3-phosphate dehydrogenase.
 Streptococcus agalactiae, and
 Streptococcus infant.
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 NCBI_TaxID=1311, 1346;
 [1]
 SEQUENCE FROM N.A.
 SPECIES=S. agalactiae, and S. infant; STRAIN=ATCC 27541, and 9117;
 RA Fontaine M.C., Perez-Casal J., Song X.-W., Shelford J., Wallison P.J.,
 Potter A.A.;
 "Immunization of dairy cattle with recombinant GapC and chimeric CAMP
 antigens confers protection against heterologous challenge with
 Streptococcus uberis.";
 Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases
 -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 DEHYDROGENASE FAMILY.
 EMBL: AF421899; AAM73770.1; -
 EMBL: AF421902; AAM73773.1; -
 GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IEA.
 GO: GO:0016491; F:oxidoreductase activity; IEA.
 GO: GO:0006096; P:glycolysis; IEA.
 InterPro: IPR006424; GAPDH-1.
 InterPro: IPR00173; GAP_dhdrogenase.
 Pfam: PF02800; gpdh. C. 1.
 PRINTS: PR00078; G3PDHGNASE.
 TIGRFAMs: TIGR01534; GAPDH-1; 1.
 PROSITE: PS00071; GAPDH. 1.
 Oxidoreductase.
 SEQUENCE 336 AA; 35723 MW; ABA9E14F3ED111 CRC64;

Query Match 92.4%; Score 1584; DB 2; Length 336;
 Best Local Similarity 90.5%; Pred. No. 3.4e-98;
 Matches 304; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

1 M V V K G I N G F R I G R I A F R I O N V G E V T R I N D L T D P M L A H L K Y D T T G R F D G T V E V 60
 1 M V V K V I N G F R I G R I A F R I O N V G E V T R I N D L T D P M L A H L K Y D T T G R F D G T V E V 60
 61 K E G F E V N G F I K V S A R D E P N I M A T D G V E I V L E A T G F P A K K A A E K H L H A N G A K K V I 120
 61 K O G F E V N G S F V K V S A R E P A N I D M A T D G V I L E A T G F P A K K A A O H H A N G A K K V I 120
 121 T A P G S N D V K V V N T N H D I L D G T E V I S G A S C T T N C L A P M A K L H D A F G I O K G I M T T H A 180
 121 T A P G S N D V K V V N T N H D I L D G T E V I S G A S C T T N C L A P M A K L H D A F G I O K G I M T T H A 180
 181 Y T G D Q M I L D G P H R G D L R R A R A G A N I V P N S T G A A K A I G L V I P E I N G K L D G A A Q R V P V P T 240
 181 Y T G D Q M I L D G P H R G D L R R A R A G A N I V P N S T G A A K A I G L V I P E I N G K L D G A A Q R V P V P T 240
 241 G S V T E L V A V L E K T S V E E I N A M A K A A N D S F G T E D P I V S S D I V G S G L F D A T Q T K V 300
 241 G S V T E L V A V L E K T S V E E I N A M A K A A N D S F G T E D P I V S S D I V G S G L F D A T Q T K V 300
 301 E V D S Q L V K V S W D N E M S Y T A Q L V R T L E F A K I A K 336
 301 T V D S Q L V K V S W D N E M S Y T A Q L V R T L E F A K I A K 336

RESULT 10
 08DVY3 PRELIMINARY; PRT; 337 AA.
 08DVY3
 AC 08DVY3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 Extracellular glyceraldehyde-3-phosphate dehydrogenase [EC
 1.2.1.12]
 GAPC OR SKD.360.

CS Streptococcus mutans. Lactobacillales; Streptococcaceae;
CC Bacteria; Firmicutes; Streptococcaceae;
OC Streptococcus;
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Qian Y.,
Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT Genome sequence of Streptococcus mutans UA159, a cariogenic dental
pathogen.
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL: A501483; A501483.1;
DR GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.
DR GO: GO:0016491; E:oxidoreductase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR006424; CAPDH-I.
DR InterPro: IPR00173; GAP_dhydrogenase.
DR Pfam: PF00044; gpdh_1.
DR Pfam: PF02800; gpdh_C_1.
DR PRINTS: PR00078; G3PDHGNASE.
DR TIGRFBMS: TIGR01534; GAPDH-I; 1.
DR PROSITE: PS00071; GAPDH; 1.
KM Oxidoreductase; Complete proteome.
SQ SEQUENCE 337 AA; 36068 MW; 42BFE20165963C22 CRC64;

Query Match 92.1%; Score 1579.5; DB 16; Length 337;
Best Local Similarity 90.2%; Pred. No. 6.9e-98;
Matches 304; Conservative 18; Mismatches 14; Indels 1; Gaps 1;

QY 1 M V V K G I N G R G R I G L A F R I O N V E G V T R I N D L T D P N M L A H L K Y D T T G R P D G T V E V 60
DB 1 M V V K G I N G R G R I G L A F R I O N V E G V T R I N D L T D P N M L A H L K Y D T T G R P D G T V E V 60
QY 61 K E G F E V N G N F I K Y S A R D P E N I D A T G V E I V E A T G F P A K K A A K H L H N G A K K V I 119
DB 61 K E G F E V N G N F I K Y S A R D P E N I D A T G V E I V E A T G F P A K K A A K H L H N G A K K V I 120
QY 120 T A P G S N D V K T V E N T N H D I D G T E T V I S G A S C T T K C L A P A K A L H D A F G I O G M T T I H 179
DB 121 T A P G S N D I K T I V E N T N H D I D G T E T V I S G A S C T T K C L A P A K A L H N F S I X G M T T I H 180
QY 180 A T T G O M T I D G P R G G D L R P A R A G A N T I V N S T G A A K A I G V I P E L N G K I D G A A Q R V P P T 239
DB 181 A T T G O M T I D G P R G G D L R P A R A G A N T I V N S T G A A K A I G V I P E L N G K I D G A A Q R V P P T 240
QY 240 T S G V T E L V T L D K N V S V D E I N A M K A S N D S F G Y E D P I V S S D I V G S Y S L P D A T O T K V 299
DB 241 T S G V T E L V A V I D K T V I D E V N A M K A A N S E Y G T E D P I V S S D I V G S F S L P D A T O T K V 300
QY 300 M E V D S Q L V K V S W Y N E M S Y T A Q V R T L E Y F A K I A K 336
DB 301 I V D K G Q L V K V S W Y N E M S Y T S Q V R T L E Y F A K I A K 337

RESULT 11
Q8KVU5 PRELIMINARY; PRT; 336 AA.
ID Q8KVU5
AC Q8KVU5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase.
OS Streptococcus parvulus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1348;
RN [1]
RP SEQUENCE FROM N.A.
RA Fontaine M.C., Perez-Casal J., Song X.-M., Shelford J., Willson P.J.,
Potter A.A.;

RT "Immunization of dairy cattle with recombinant GapC and chimeric CAMP
RT antigens confers protection against heterologous challenge with
RT Streptococcus uberis.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL: AF421901; AAM73772.1;
DR GO: GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.
DR GO: GO:0016491; E:oxidoreductase activity; IEA.
DR GO: GO:0006096; P:glycolysis; IEA.
DR InterPro: IPR006424; GAPDH-I.
DR InterPro: IPR00173; GAP_dhydrogenase.
DR Pfam: PF00044; gpdh_1.
DR Pfam: PF02800; gpdh_C_1.
DR PRINTS: PR00078; G3PDHGNASE.
DR TIGRFBMS: TIGR01534; GAPDH-I; 1.
DR PROSITE: PS00071; GAPDH; 1.
KM Oxidoreductase.
SQ SEQUENCE 336 AA; 36037 MW; 311647C25489AC9E CRC64;

Query Match 92.0%; Score 1578; DB 2; Length 336;
Best Local Similarity 90.8%; Pred. No. 8.6e-98;
Matches 305; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 M V V K G I N G R G R I G L A F R I O N V E G V T R I N D L T D P N M L A H L K Y D T T G R P D G T V E V 60
DB 1 M V V K G I N G R G R I G L A F R I O N V E G V T R I N D L T D P N M L A H L K Y D T T G R P D G T V E V 60
QY 61 K E G F E V N G N F I K Y S A R D P E N I D A T G V E I V E A T G F P A K K A A K H L H N G A K K V I 120
DB 61 K D G F V D N K P L K Y S A R D P E N I D A T G V E I V E A T G F P A K K A A K H L H N G A K K V I 120
QY 121 T A P G S N D V K T V E N T N H D I D G T E T V I S G A S C T T K C L A P A K A L H D A F G I O G M T T I H 180
DB 121 T A P G S N D V K T V E N T N H D I D G T E T V I S G A S C T T K C L A P A K A L H N F S I X G M T T I H 180
QY 181 Y T G D M I D G P R G G D L R P A R A G A N T I V N S T G A A K A I G V I P E L N G K I D G A A Q R V P P T 240
DB 181 Y T G D M I D G P R G G D L R P A R A G A N T I V N S T G A A K A I G V I P E L N G K I D G A A Q R V P P T 240
QY 241 G S V T E L V T L D K N V S V D E I N A M K A S N D S F G Y E D P I V S S D I V G S Y S L P D A T O T K V 300
DB 241 G S V T E L V A V I D K T V I D E V N A M K A A N S E Y G T E D P I V S S D I V G S F S L P D A T O T K V 300
QY 301 E V D S Q L V K V S W Y N E M S Y T A Q V R T L E Y F A K I A K 336
DB 301 T V D G N Q L V K V S W Y N E M S Y T A Q V R T L E Y F A K I A K 336

RESULT 12
Q8VVB9 PRELIMINARY; PRT; 336 AA.
ID Q8VVB9
AC Q8VVB9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase.
GN GAPDH.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMG1831;
RA van den Bogard P.T.C., Kleerebezem M., Hols P., Crispie F.,
Knijpers O.P., de Vos W.M.;
RT "Modulation of glycolysis by lactose availability in Streptococcus
RT thermophilus.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.
DR EMBL: AF442551; AAL35177.1;

DR HSP; P00354; 3SPD.
 DR GO; GO:0004365; F:glyceralddehyde-3-phosphate dehydrogenase (p. . .); IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR006424; GAPDH-1.
 DR InterPro; IPR000173; GAP_dhrogenase.
 DR Pfam; PF00044; gpdh; 1.
 DR Pfam; PF02800; gpdh C; 1.
 DR PRINTS; PR00078; G3PDHGNASE.
 DR TIGRfams; TIGR01534; GAPDH-1; 1.
 DR PROSITE; PS00071; GAPDH; 1.
 DR Oxidoreductase.
 SQ SEQUENCE 336 AA; 36026 MW; 52C1F25F3A7E0230 CRC64;

Query Match 91.7%; Score 1572; DB 2; Length 336;
 Best Local Similarity 90.2%; Pred. No. 2.2e-97;
 Matches 303; Conservative 18; Mismatches 15; Indels 0; Gaps 0;

QY 1 WYKVGNGFGRIGLAFRIQVGEVTRINDLDPNMLAHLYKDTTQGRPDGTVEV 60
 DB 1 WYKVGNGFGRIGLAFRIQVGEVTRINDLDPNMLAHLYKDTTQGRPDGTVEL 60
 QY 61 KEGFEVNGFIVSARDEPENIDWATDGEIVLBATGFPAKKAERKILHAGAKKVI 120
 DB 61 KEGFEVNGFIVSARDEPENIDWATDGEIVLBATGFPAKKAERKILHAGAKKVI 120
 QY 121 TAPGANTVTVFNTNHDLDGTETVSGASTCTNCCLAPMAKALHAPGJOKGIMTTIHA 180
 DB 121 TAPGANTVTVFNTNHDLDGTETVSGASTCTNCCLAPMAKALHAPGJOKGIMTTIHA 180
 QY 181 YTGDMILDGPRRGDRLRARAAGANIVPNSGAAKAGIVIPELNGKLDGAAGRPVPT 240
 DB 181 YTGDMILDGPRRGDRLRARAAGANIVPNSGAAKAGIVIPELNGKLDGAAGRPVPT 240
 QY 241 GSYTELVTLDKNSVDEINAAKASNDSPGTEDPIVSSDIYVSGSLFDATQTKWEVD 300
 DB 241 GSYTELVAECNKVTVDEVNAAKASNDSPGTEDPIVSSDIYVSGSLFDATQTKVL 300
 QY 301 EYDSQGLVYVSWYDNEASYTAOLVRLTEYFAKIK 336
 DB 301 DVDGKQLVKVSMTDNEASYTSQVRLTEYFAKIK 336

RESULT 13
 Q9LSX6 PRELIMINARY; PRT; 320 AA.

AC Q9LSX6; PRELIMINARY; PRT; 320 AA.
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Extracellular glyceralddehyde-3-phosphate dehydrogenase (Fragment).
 OS Streptococcus gordonii.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1302;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nelson D., Goldstein J.M., Boatright K., Hartly D.W.S., Cook S.L.,
 RA Hickman P.J., Potempa J., Travis J., Mayo J.A.;
 RT "Purification and characterization of an extracellular
 glyceralddehyde-3-phosphate dehydrogenase from Streptococcus sanguis
 and cloning of the gene encoding this enzyme."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 DEHYDROGENASE FAMILY.
 CC EMBL; AF247678; AAF64063.1; -.
 DR HSP; P00362; 1GD1.
 DR GO; GO:0004365; F:glyceralddehyde-3-phosphate dehydrogenase (p. . .); IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR006424; GAPDH-1.
 DR InterPro; IPR000173; GAP_dhrogenase.

DR Pfam; PF00044; gpdh; 1.
 DR Pfam; PF02800; gpdh C; 1.
 DR PRINTS; PR00078; G3PDHGNASE.
 DR TIGRfams; TIGR01534; GAPDH-1; 1.
 DR PROSITE; PS00071; GAPDH; 1.
 KW Oxidoreductase.
 FT MON TER 1 1
 FT NON TER 320 320
 SQ SEQUENCE 320 AA; 33968 MW; 6FCC18BB01E91F0 CRC64;

Query Match 88.5%; Score 1518; DB 2; Length 320;
 Best Local Similarity 91.2%; Pred. No. 8.4e-94;
 Matches 292; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 4 KVGNGFGRIGLAFRIQVGEVTRINDLDPNMLAHLYKDTTQGRPDGTVEVKSG 63
 DB 1 KVGNGFGRIGLAFRIQVGEVTRINDLDPNMLAHLYKDTTQGRPDGTVEVKSG 60
 QY 64 GFEVNGFIVSARDEPENIDWATDGEIVLBATGFPAKKAERKILHAGAKKVI 123
 DB 61 GFEVNGFIVSARDEPENIDWATDGEIVLBATGFPAKKAERKILHAGAKKVI 120
 QY 124 GENDVTVFNTNHDLDGTETVSGASTCTNCCLAPMAKALHAPGJOKGIMTTIHA 183
 DB 121 GSDVTVFNTNHDLDGTETVSGASTCTNCCLAPMAKALHAPGJOKGIMTTIHA 180
 QY 184 DQMLDGPRRGDRLRARAAGANIVPNSGAAKAGIVIPELNGKLDGAAGRPVPTGSV 243
 DB 181 DQMLDGPRRGDRLRARAAGANIVPNSGAAKAGIVIPELNGKLDGAAGRPVPTGSV 240
 QY 244 TELVTLDNVSVDEINAAKASNDSPGTEDPIVSSDIYVSGSLFDATQTKWEVD 303
 DB 241 TELVTLDNVSVDEINAAKASNDSPGTEDPIVSSDIYVSGSLFDATQTKVIDVD 300
 QY 304 GSGLVKVSMTDNEASYTAQ 323
 DB 301 GSGLVKVSMTDNEASYTAQ 320

RESULT 14
 Q9ALT7 PRELIMINARY; PRT; 309 AA.

AC Q9ALT7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glyceralddehyde-3-phosphate dehydrogenase (BC 1.2.1.12) (Fragment).
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=clinical isolate;
 RA Amezaga M.R., Carter P.E., McKenzie H.;
 RT "Sequence variation in mef(A) and gap genes in M-phenotype
 erythromycin resistant Streptococcus pneumoniae";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 DEHYDROGENASE FAMILY.
 CC EMBL; AJ292048; CAC27448.1; -.
 DR HSP; P00362; 1GD1.
 DR GO; GO:0004365; F:glyceralddehyde-3-phosphate dehydrogenase (p. . .); IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR InterPro; IPR006424; GAPDH-1.
 DR InterPro; IPR000173; GAP_dhrogenase.
 DR Pfam; PF00044; gpdh; 1.
 DR Pfam; PF02800; gpdh C; 1.
 DR PRINTS; PR00078; G3PDHGNASE.
 DR TIGRfams; TIGR01534; GAPDH-1; 1.

DR PROSITE: PS00071; GAPDH; 1.
 KM Oxidoreductase.
 FT NON_TER 1
 FT NON_TER 309
 SQ SEQUENCE 309 AA; 32930 MW; 89E45C3BEA6A0528 CRC64;

Query Match 85.6%; Score 1468.5; DB 2; Length 309;
 Best Local Similarity 91.9%; Pred. No. 1.7e-90;
 Matches 285; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 9 GFGRIGLAERRIQVEGEVETRIINDLDPNMLAHILKVDITQGRFDGVEVKGSGFEVN 68
 DB 1 GFGRIGLAERRIQVEGEVETRIINDLDPNMLAHILKVDITQGRFDGVEVKGSGFEVN 60
 QY 69 GNFIVSAERDPENIDMATDGEIVLEATGFPAAKEAELHANAKKVVITAPGANDV 128
 DB 61 GNFIVSAERDPENIDMATDGEIVLEATGFPAAKEAELHANAKKVVITAPGANDV 113
 QY 129 KTVFNTNHDITDGETEVTISGASCTTNCLAPAKALHDAFGIQRKGLMTTHAYTGDMIL 188
 DB 120 KTVFNTNHDITDGETEVTISGASCTTNCLAPAKALHDAFGIQRKGLMTTHAYTGDMIL 179
 QY 189 DGFHGGDLRRARAGANIVPNSGAAKALGLVPELNGKLDGAQRVPPTGVTETLV 248
 DB 180 DGFHGGDLRRARAGANIVPNSGAAKALGLVPELNGKLDGAQRVPPTGVTETLV 239
 QY 249 TLDRKVSDEINAAKASNDSEGTEDPIVSSDIYGVSYGSLFDATQTKMEYDSGLV 308
 DB 240 VLEKXVTVDEVNAAKKAASNESYGTEDPIVSSDIYGVSYGSLFDATQTKVLDVGRQLV 299
 QY 309 KVSMTDNEM 318
 DB 300 KVSMTDNEM 309

RESULT 15

Q9AJT9 PRELIMINARY; PRT; 309 AA.

AC Q9AJT9;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
 IE (Fragment).
 GX GAP.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxId=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=clinical isolate;
 RA Amezcua M.R., Carter P.E., Cash P., McKenzie H.;
 RT "Sequence variation in mef(A) and gap genes in M-phenotype
 erythromycin resistant Streptococcus pneumoniae."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 DEHYDROGENASE FAMILY.
 CC EMBL: AJ292046; CAC7446.1; -;
 DR HSESP; P00362; IGD1.
 DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IBA.
 DR GO; GO:0016491; F:oxidoreductase activity; IBA.
 DR GO; GO:0006096; P:glycolysis; IBA.
 DR InterPro: IPR006424; GAPDH-I.
 DR InterPro: IPR001173; GAP_dhdcgenase.
 DR Pfam: PF00044; spdh_1.
 DR Pfam: PF02800; spdh_C_1.
 DR PRINTS: PR00078; GAPDHGNASE.
 DR TIGRFAMs: TIGR01534; GAPDH-I; 1.
 DR PROSITE: PS00071; GAPDH; 1.
 KM Oxidoreductase.
 FT NON_TER 1
 FT NON_TER 309

SQ SEQUENCE 309 AA; 32916 MW; 39E9CC3BEA6F8959 CRC64;

Query Match 85.6%; Score 1467.5; DB 2; Length 309;
 Best Local Similarity 91.6%; Pred. No. 1.7e-90;
 Matches 284; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 9 GFGRIGLAERRIQVEGEVETRIINDLDPNMLAHILKVDITQGRFDGVEVKGSGFEVN 63
 DB 1 GFGRIGLAERRIQVEGEVETRIINDLDPNMLAHILKVDITQGRFDGVEVKGSGFEVN 60
 QY 69 GNFIVSAERDPENIDMATDGEIVLEATGFPAAKEAELHANAKKVVITAPGANDV 128
 DB 61 GNFIVSAERDPENIDMATDGEIVLEATGFPAAKEAELHANAKKVVITAPGANDV 119
 QY 129 KTVFNTNHDITDGETEVTISGASCTTNCLAPAKALHDAFGIQRKGLMTTHAYTGDMIL 188
 DB 120 KTVFNTNHDITDGETEVTISGASCTTNCLAPAKALHDAFGIQRKGLMTTHAYTGDMIL 179
 QY 189 DGFHGGDLRRARAGANIVPNSGAAKALGLVPELNGKLDGAQRVPPTGVTETLV 248
 DB 180 DGFHGGDLRRARAGANIVPNSGAAKALGLVPELNGKLDGAQRVPPTGVTETLV 239
 QY 249 TLDRKVSDEINAAKASNDSEGTEDPIVSSDIYGVSYGSLFDATQTKMEYDSGLV 308
 DB 240 VLEKXVTVDEVNAAKKAASNESYGTEDPIVSSDIYGVSYGSLFDATQTKVLDVGRQLV 299
 QY 309 KVSMTDNEM 318
 DB 300 KVSMTDNEM 309

Search completed: May 5, 2004, 14:21:09
 Job time : 46 secs

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CM protein - protein search, using sw model

Run on: May 5, 2004, 14:12:18 ; Search time 59 Seconds
(without alignments)
1609.084 Million cell updates/sec

Title: US-09-878-781-4
Perfect score: 1715
Sequence: 1 MVYKVGNGFRIGRLAERR.....EMSYTAQVLTLEYFAKIAK 336

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

- 1: Geneseq19808:*
- 2: Geneseq19908:*
- 3: Geneseq20008:*
- 4: Geneseq20018:*
- 5: Geneseq20028:*
- 6: Geneseq20038:*
- 7: Geneseq20038:*
- 8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1715	100.0	336	5	AAM50665 Streptococcus
2	1715	100.0	336	5	AAM50639 Streptococcus
3	1714	99.9	336	5	ABP29960 Streptococcus
4	1714	99.9	336	6	ABU46455 Streptococcus
5	1714	99.9	345	5	ABP29106 Streptococcus
6	1711	99.8	336	2	AAR56486 Streptococcus
7	1711	99.8	336	4	AAV85681 Streptococcus
8	1656.5	96.6	448	5	AAM50664 Streptococcus
9	1618	94.3	336	5	AAM50667 Streptococcus
10	1618	94.3	336	5	AAM50641 Streptococcus
11	1609	93.8	336	5	ABP30758 Streptococcus
12	1602	93.4	336	5	AAM50666 Streptococcus
13	1602	93.4	336	5	AAM50640 Streptococcus
14	1593.5	92.9	336	6	ABU02516 Streptococcus
15	1593.5	92.9	359	4	AAU37576 Streptococcus
16	1593.5	92.9	359	6	ABU46262 Streptococcus
17	1592.5	92.9	359	4	AAU38000 Streptococcus
18	1584	92.4	336	5	AAM50669 Streptococcus
19	1584	92.4	336	5	AAM50643 Streptococcus
20	1579.5	92.1	337	6	ABU44330 Streptococcus
21	1578	92.0	336	5	AAM50668 Streptococcus
22	1578	92.0	336	5	AAM50642 Streptococcus
23	1549.5	90.3	333	2	AAM50689 Streptococcus
24	1549.5	90.3	333	5	ABP34583 Streptococcus
25	1549.5	90.3	333	7	ADG45135 Streptococcus

26	1410	82.2	336	5	ABM55601 Lactococcus
27	1337.5	78.0	333	4	AAU35254 Streptococcus
28	1337.5	78.0	333	6	ABU29370 Streptococcus
29	1333.5	77.8	336	5	ABM55868 Streptococcus
30	1325.5	77.3	333	7	AUC35142 Streptococcus
31	1277	74.5	335	5	ABU25342 Streptococcus
32	1262	73.6	336	5	ABM48810 Streptococcus
33	1262	73.6	336	5	ABU32568 Streptococcus
34	1259.5	73.4	334	6	ABU23595 Streptococcus
35	1217.5	71.0	335	6	ABU43810 Streptococcus
36	1197.5	69.8	334	6	ABU37737 Streptococcus
37	1196.5	69.8	357	6	ABP81005 Streptococcus
38	1196.5	69.8	357	6	ABU37077 Streptococcus
39	1190	69.4	336	4	AAU383058 Streptococcus
40	1190	69.4	336	5	ABU42966 Streptococcus
41	1190	69.4	348	5	ABP40668 Streptococcus
42	1183	69.0	336	4	AAU36947 Streptococcus
43	1183	69.0	336	4	AAU34122 Streptococcus
44	1183	69.0	336	6	ABU19195 Streptococcus
45	1183	69.0	336	6	ABU16073 Streptococcus

ALIGNMENTS

RESULT 1
ID AAM50665 standard; protein; 336 AA.
XX AAM50665;
XX AC AAM50665;
XX DT 08-APR-2002 (first entry)
XX DE Streptococcus dysgalactiae gapC plasmid binding protein DysGapC.
XX DM Streptococcus dysgalactiae gapC plasmid binding protein; epitope; infection; vaccine;
XX RW Immunisation; mastitis; therapy.
XX CS Streptococcus dysgalactiae.
XX FN W0200196379-A2.
XX PD 20-DEC-2001.
XX PF 11-JUN-2001; 2001MO-CA000836.
XX PR 12-JUN-2000; 2000US-0211247P.
XX PA (UYSA-) UNIV SASKATCHEWAN.
XX PI Potter AA, Perez-Casal J, Fontaine M;
XX DR WPI; 2002-098051/13.
XX DR N-PSDB; ABN91328.
XX PT Novel gapC multiple epitope fusion polypeptide comprising antigenic
XX PT determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, S.
XX PT parviteris, or S. iniae gapC protein useful for treating mastitis in
XX PT vertebrates.
XX PS Claim 8; Fig 1A-B; 11epp; English.
XX CC The present sequence is that of the gapC plasmid binding protein,
XX CC DysGapC, of Streptococcus dysgalactiae ATCC 43078, an isolate from a case
XX CC of bovine mastitis. The invention relates to novel gapC multiple epitope
XX CC fusion proteins that comprise epitopes from 1 or more of Streptococcus
XX CC dysgalactiae, Streptococcus agalactiae, Streptococcus parviteris,
XX CC Streptococcus uberis and Streptococcus iniae (see AAM50665-69). A claimed
XX CC example is PolyGapC (see AAM50664). Expression vectors and host cells for
XX CC production of the multiple epitope fusion proteins are provided. The
XX CC multiple epitope proteins are used in claimed vaccines for treating or
XX CC preventing a bacterial infection in a vertebrate, especially a
XX CC streptococcal infection, and particularly mastitis. They are also used in

PI Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C;
PI Tetelin H;
XX WPI; 2002-352536/38.
DR N-PSDB; ABN70591.
XX
XX New Streptococcus protein for the treatment or prevention of infection or
PT disease caused by Streptococcus bacteria, such as meningitis, and for
PT detecting a compound that binds to the protein.
XX
XX Claim 1; Page 4011; 4525pp; English.
XX
CC The invention relates to a protein (ABP25413-ABP20895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and anti-inflammatory
CC activity. (1), nucleic acids encoding (1), ABN60044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) is used to determine whether a compound binds to
CC a biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 336 AA;
Query Match 99.9%; Score 1714; DB 5; Length 336;
Best Local Similarity 99.7%; Pred. No. 1.1e-144;
Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYVKGINGFGRIAGRIAPRIQNGVEVTRINDLDPMLAHILKDTTQGRFGTVEV 60
DB 1 MYVKGINGFGRIAGRIAPRIQNGVEVTRINDLDPMLAHILKDTTQGRFGTVEV 60
QY 61 KEGGFVNGNFIKVSARDEPNIDMTDGEIVLEATGFPAAKKAERKHLHANGAKKVI 120
DB 61 KEGGFVNGNFIKVSARDEPNIDMTDGEIVLEATGFPAAKKAERKHLHANGAKKVI 120
QY 121 TARGNDKKTVEVNTNDILDGTEVIVSGASCTTNCLAPMARALHDAFGIOKELMTTHA 180
DB 121 TARGNDKKTVEVNTNDILDGTEVIVSGASCTTNCLAPMARALHDAFGIOKELMTTHA 180
QY 181 YTGDDWILDGHRGGDARRARAGANITVPNSTGAANAIGLVPILNGKLDGAARVPVT 240
DB 181 YTGDDWILDGHRGGDARRARAGANITVPNSTGAANAIGLVPILNGKLDGAARVPVT 240
QY 241 GSVTELVYTLTKNVSVEIINAAKASNDSPGYTEPIVSDIVSGYSLFATYTKVM 300
DB 241 GSVTELVYTLTKNVSVEIINAAKASNDSPGYTEPIVSDIVSGYSLFATYTKVM 300
QY 301 EYDGSQLYKVSWSYDNEMSTYTAQVTRTEFPATKAK 336
DB 301 EYDGSQLYKVSWSYDNEMSTYTAQVTRTEFPATKAK 336
QY 301 EYDGSQLYKVSWSYDNEMSTYTAQVTRTEFPATKAK 336
DB 301 EYDGSQLYKVSWSYDNEMSTYTAQVTRTEFPATKAK 336
RESULT 4
ABU46455
ID ABU46455 standard; protein; 336 AA.
XX
XX ABU46455;
AC
XX
XX 19-JUN-2003 (first entry)
DT
XX
XX Protein encoded by Prokaryotic essential gene #31982.
DE
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW
XX

OS Streptococcus pyogenes.
XX
XX MO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITTA PHARM INC.
XX
XX Wang J, Zamudio C, Malone C, Haeelbeck R, Ohlsen KU, Zykink JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI: 2003-029926/02.
XX N-PSDB; ACA50325.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 74379; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 623 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-regulated gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 336 AA;
Query Match 99.9%; Score 1714; DB 6; Length 336;
Best Local Similarity 99.7%; Pred. No. 1.1e-144;
Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYVKGINGFGRIAGRIAPRIQNGVEVTRINDLDPMLAHILKDTTQGRFGTVEV 60
DB 1 MYVKGINGFGRIAGRIAPRIQNGVEVTRINDLDPMLAHILKDTTQGRFGTVEV 60
QY 61 KEGGFVNGNFIKVSARDEPNIDMTDGEIVLEATGFPAAKKAERKHLHANGAKKVI 120
DB 61 KEGGFVNGNFIKVSARDEPNIDMTDGEIVLEATGFPAAKKAERKHLHANGAKKVI 120

QY 121 TAPGNDVKTWVNTNHDILDGTEVTSIGASCTTNCLAPAKALHDARFQIGLMTTTHA 180
 DB 121 TAPGNDVKTWVNTNHDILDGTEVTSIGASCTTNCLAPAKALHDARFQIGLMTTTHA 180
 QY 181 YTGDMITLDGPHRGDLPARAGANIVPNSGAKAIGLVIPINCKLDGAORVPVPT 240
 DB 181 YTGDMITLDGPHRGDLPARAGANIVPNSGAKAIGLVIPINCKLDGAORVPVPT 240
 QY 241 GSVELVITLIDKXVSVDENINAKKAASNDSPGYTEDPIVSSDIVGVSGLPDAQTCKM 300
 DB 241 GSVELVITLIDKXVSVDENINAKKAASNDSPGYTEDPIVSSDIVGVSGLPDAQTCKM 300
 QY 301 EVDGSQLVKVSWYDNEMSYTAQVLTLEYFAKIAK 336
 DB 301 EVDGSQLVKVSWYDNEMSYTAQVLTLEYFAKIAK 336

RESULT 5

ABP29106
 ID ABP29106 standard; protein; 345 AA.

AC ABP29106;

DT 02-JUL-2002 (first entry)

DE Streptococcus polypeptide SEQ ID NO 7388.

KM Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KM group A streptococcus; Streptococcus pyogenes; antibacterial;

KM antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus pyogenes.

XX W0230234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

XX 24-NOV-2000; 2000GB-00028727.

XX 07-MAR-2001; 2001GB-00035640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford C, Masigrani V, Margarit Y Rosi, Grandi G, Fraser C;

XX Tettein H;

XX MPI; 2002-352536/38.

XX N-PSDB; ABN69737.

XX Claim 1; Page 3888; 4525pp; English.

CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be

CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins

XX Sequence 345 AA;

Query Match 99.94; Score 1714; DB 5; Length 345;
 Best Local Similarity 99.74; Pred. No. 1,1e-144;
 Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVKGINFGRIQGLAPRIQWEGVETRLINDLTDPNMLAHLKYDTGGRDGVVEV 60
 DB 10 MYVKGINFGRIQGLAPRIQWEGVETRLINDLTDPNMLAHLKYDTGGRDGVVEV 69
 QY 61 KEGFEVNGNFIKVSAEDPENIDMATDGEVLEIATGFPKKEAAEKHLNAGAKKVI 120
 DB 70 KEGFEVNGNFIKVSAEDPENIDMATDGEVLEIATGFPKKEAAEKHLNAGAKKVI 129
 QY 121 TAPGNDVKTWVNTNHDILDGTEVTSIGASCTTNCLAPAKALHDARFQIGLMTTTHA 180
 DB 130 TAPGNDVKTWVNTNHDILDGTEVTSIGASCTTNCLAPAKALHDARFQIGLMTTTHA 189
 QY 181 YTGDMITLDGPHRGDLPARAGANIVPNSGAKAIGLVIPINCKLDGAORVPVPT 240
 DB 190 YTGDMITLDGPHRGDLPARAGANIVPNSGAKAIGLVIPINCKLDGAORVPVPT 249
 QY 241 GSVELVITLIDKXVSVDENINAKKAASNDSPGYTEDPIVSSDIVGVSGLPDAQTCKM 300
 DB 250 GSVELVITLIDKXVSVDENINAKKAASNDSPGYTEDPIVSSDIVGVSGLPDAQTCKM 309
 QY 301 EVDGSQLVKVSWYDNEMSYTAQVLTLEYFAKIAK 336
 DB 310 EVDGSQLVKVSWYDNEMSYTAQVLTLEYFAKIAK 345

RESULT 6

AAR56486
 ID AAR56486 standard; protein; 336 AA.

AC AAR56486;

DT 25-MAR-2003 (revised)

DT 22-FEB-1995 (first entry)

DE Plasmin receptor.

KM Plasmin receptor; isolate 64/14; plasmin; alpha-2-antiplasmin;

KM plasminogen activator; bleeding; reocclusion; thrombosis;

KM pulmonary embolism; clots.

XX Streptococcus pyogenes.

XX US5328996-A.

XX 10-AUG-1992; 92US-00928462.

XX 29-MAR-1989; 89US-00330849.

XX 16-MAY-1990; 90US-00524411.

XX (UYFL) UNIV FLORIDA RES FOUND INC.

XX Von Mering G, Broder C, Boyle MDP, Lottenberg R;

XX MPI; 1994-225327/27.

XX N-PSDB; AAQ70705.

CC New DNA encoding bacterial plasmin receptor - useful as thrombolytic
 CC agents, used with plasminogen activator or bound to plasmin, also useful
 CC in vaccines against bacterial infection.
 PS Claim 1; Col 27-30; 19pp; English.

XX This sequence represents the S. pyogenes plasmin receptor. The DNA
 CC encoding this sequence was isolated from the S. pyogenes clinical isolate
 CC 64/14. The plasmin receptor has a very high affinity for plasmin which,
 CC when bound, retains its enzymatic activity but is not regulated
 CC (inhibited) by alpha-2-antiplasmin. The receptor protein, when
 CC administered concurrently or sequentially, prolongs the activity of
 CC plasminogen activator (PA) so allows a reduction in dose, and thus lowers
 CC the risk of bleeding, and may prevent recocclusion of blood vessels. The
 CC protein may be coupled to a fibrin-specific monoclonal antibody to
 CC provide targeting to clots. The plasmin receptor may be useful in human
 CC or veterinary medicine, for treatment of thrombosis and pulmonary
 CC embolism, and for solubilizing clots in catheters or shunts. (Updated on
 CC 25-MAR-2003 to correct PF field.)
 XX

Sequence 336 AA;

Query Match 99.8%; Score 1711; DB 2; Length 336;

Best Local Similarity 99.4%; Pred. No. 2e-144;
 Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVKGINGFRIGRLAFRIQNVGVEVTRINDLTDPMMLAHLLKDTTQGRPDGTVYV 60
 DB 1 MYVKGINGFRIGRLAFRIQNVGVEVTRINDLTDPMMLAHLLKDTTQGRPDGTVYV 60
 QY 61 KEGFEVNGNFIKVSABRPENIDMATDVEIVLATGFEAKKEAKHLHANGAKKVI 120
 DB 61 KEGFEVNGNFIKVSABRPENIDMATDVEIVLATGFEAKKEAKHLHANGAKKVI 120
 QY 121 TAPGNDVKTVEVNTNHDILDTGTVISGASCTTNCIAPMAKALHDAFGIQKGLMTTHA 180
 DB 121 TAPGNDVKTVEVNTNHDILDTGTVISGASCTTNCIAPMAKALHDAFGIQKGLMTTHA 180
 QY 181 YTGDDMIIDGPHRGGLRRARAGANIVPNSGAAKALGLVPELNGSLDGAQRVPPT 240
 DB 181 YTGDDMIIDGPHRGGLRRARAGANIVPNSGAAKALGLVPELNGSLDGAQRVPPT 240
 QY 241 GSVELVLTLDKNVSYDEINAAKASNDSPGYTDPVSSDIIVGYSGLPDAQTQYV 300
 DB 241 GSVELVLTLDKNVSYDEINAAKASNDSPGYTDPVSSDIIVGYSGLPDAQTQYV 300
 QY 301 EVDGSQLVKKVSWYDNEMSYTAQLVRLTEYPAKIAK 336
 DB 301 EVDGSQLVKKVSWYDNEMSYTAQLVRLTEYPAKIAK 336

RESULT 7

AA85681
 ID AA85681 standard; protein; 336 AA.

XX
 AC AA85681;

XX
 DT 13-FEB-2001 (first entry)

XX
 DE Streptococcal plasmin receptor amino acid sequence.

XX
 KW Plasmin receptor; p1r; immune response; vaccination; antibacterial;
 KW Streptococcal infection; antihelminthic.

XX
 OS Streptococcus pyogenes.

XX
 PN US613623-A.

XX
 PD 24-OCT-2000.

XX
 PF 11-JUL-1994; 94US-00273247.

XX
 PR 29-MAR-1989; 89US-00330849.

XX
 PR 16-MAY-1990; 90US-00524411.

XX
 PR 10-AUG-1992; 92US-00928462.

XX
 PA (UTFL) UNIV FLORIDA RES FOUND INC.

P1 Von Mering G, Broder C, Lottenberg R, Boyle MDP;
 XX
 XX WPI: 2001-066210/01.
 DR N-PSDB; AAC66140.
 XX
 PT Raising an immune response in a mammal, especially for vaccination
 PT against group A streptococcal infections, comprises administering an
 PT isolated streptococcal plasmin receptor protein.

PS Claim 2; Col 27-30; 17pp; English.

XX
 XX Polynucleotide sequence AAC66140 encodes the Streptococcal plasmin
 CC receptor protein AA85681. The protein is used in a method for raising an
 CC immune response in a mammal. The method comprises administering the
 CC plasmin receptor protein. The method is useful as a vaccination against
 CC group A Streptococcal infections and potentially against a broad range of
 CC infections associated with pathogens expressing glyceraldehyde-3-
 CC phosphate dehydrogenase (GAPDH) or GAPDH-like proteins at their cell
 CC surfaces. The vaccine has antibacterial and antihelminthic activity
 CC
 XX

Sequence 336 AA;

Query Match 99.8%; Score 1711; DB 4; Length 336;

Best Local Similarity 99.4%; Pred. No. 2e-144;
 Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVKGINGFRIGRLAFRIQNVGVEVTRINDLTDPMMLAHLLKDTTQGRPDGTVYV 60
 DB 1 MYVKGINGFRIGRLAFRIQNVGVEVTRINDLTDPMMLAHLLKDTTQGRPDGTVYV 60
 QY 61 KEGFEVNGNFIKVSABRPENIDMATDVEIVLATGFEAKKEAKHLHANGAKKVI 120
 DB 61 KEGFEVNGNFIKVSABRPENIDMATDVEIVLATGFEAKKEAKHLHANGAKKVI 120
 QY 121 TAPGNDVKTVEVNTNHDILDTGTVISGASCTTNCIAPMAKALHDAFGIQKGLMTTHA 180
 DB 121 TAPGNDVKTVEVNTNHDILDTGTVISGASCTTNCIAPMAKALHDAFGIQKGLMTTHA 180
 QY 181 YTGDDMIIDGPHRGGLRRARAGANIVPNSGAAKALGLVPELNGSLDGAQRVPPT 240
 DB 181 YTGDDMIIDGPHRGGLRRARAGANIVPNSGAAKALGLVPELNGSLDGAQRVPPT 240
 QY 241 GSVELVLTLDKNVSYDEINAAKASNDSPGYTDPVSSDIIVGYSGLPDAQTQYV 300
 DB 241 GSVELVLTLDKNVSYDEINAAKASNDSPGYTDPVSSDIIVGYSGLPDAQTQYV 300
 QY 301 EVDGSQLVKKVSWYDNEMSYTAQLVRLTEYPAKIAK 336
 DB 301 EVDGSQLVKKVSWYDNEMSYTAQLVRLTEYPAKIAK 336

RESULT 8

AA850664
 ID AA850664 standard; protein; 448 AA.

XX
 AC AA850664;

XX
 DT 29-AUG-2003 (revised)

XX
 DT 08-APR-2002 (first entry)

XX
 DE Streptococcus GapC multiepitope fusion Polycap4.

XX
 KW Polycap4; GapC; plasmin binding protein; epitope; infection; vaccine;
 KW immunisation; mastitis; therapy.

XX
 OS Streptococcus dysgalactiae.

XX
 OS Streptococcus agalactiae.

XX
 OS Streptococcus parauberis.

XX
 PN WO200196379-A2.

XX
 PD 20-DEC-2001.

```

XX 11-JUN-2001; 2001MO-CA000836.
PE
XX
XX 12-JUN-2000; 2000US-0211247P.
ER
XX
XX (UTSA-) UNIV SASKATCHEWAN.
FA
XX
XX Potter AA, Perez-Casal J, Fontaine M;
PI
XX WPI; 2002-098051/13.
DR
XX N-ESDB; ABA91327.
DR
XX
XX Novel GapC multiple epitope fusion polypeptide comprising antigenic
FT determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, S.
PI parvuberis, or S. iniae GapC protein useful for treating mastitis in
FT vertebrates.
XX
XX Claim 9; Fig 6A-C; 116pp; English.
XX
XX The present sequence is that of a novel multiple epitope fusion protein,
CC designated PolyGap4, comprising the entire amino acid sequence of the
CC Streptococcus dysgalactiae GapC plasmin binding protein in addition to
CC unique amino acid sequences from the Streptococcus parvuberis and
CC Streptococcus agalactiae GapC proteins. The multiple epitope protein is
CC produced in host cells transformed with an expression vector comprising a
CC chimeric gene (see ABA91327) encoding the protein. PolyGap4 is an example
CC of novel GapC multiple epitope fusion proteins of the invention that
CC comprise epitopes from 1 or more of S. dysgalactiae, S. agalactiae, S.
CC parvuberis, Streptococcus uberis and Streptococcus iniae (see AAM50665-
CC 69). The multiple epitope fusion proteins are used in claimed vaccines
CC for treating or preventing a bacterial infection in a vertebrate,
CC especially a streptococcal infection, and particularly mastitis. They are
CC also used in claimed methods of detecting Streptococcus antibodies. The
CC multiple epitope protein is capable of eliciting broad immunity against a
CC variety of streptococcal infections while minimizing the number of
CC antigens present in the final formulation and concomitantly reducing
CC production costs. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX SQ
XX
XX Sequence 448 AA:
XX
XX Query Match 96.6%; Score 1656.5; DB 5; Length 448;
XX Best Local Similarity 79.6%; Pred. No. 2,26-139;
XX Matches 336; Conservative 0; Mismatches 1; Indels 85; Gaps 1;
XX
XX 1 MYVKVINGFGRIQLAFRRIONVEGVEVTRINDLDPNMLAHLYKDTTQGRFGTVEV 60
XX 28 MYVKVINGFGRIQLAFRRIONVEGVEVTRINDLDPNMLAHLYKDTTQGRFGTVEV 87
XX
XX 61 KEGGEVNGNFIVSAERDPE----- 81
XX
XX 88 KEGGEVNGNFIVSAERDPE----- 147
XX
XX 82 -----NIDMAGTGVIVAE 95
XX
XX 148 KDBEQIDMAGTGVIVAEIDGTVVEKGGFVNGQVKSARERPNIDMAGTGVIVAE 207
XX
XX 96 ATGFPAKKEAAKEHANGAKKVVITAPGNDVTVFWTNHDIIDGTEVIGASCTTN 155
XX 208 ATGFPAKKEAAKEHANGAKKVVITAPGNDVTVFWTNHDIIDGTEVIGASCTTN 267
XX
XX 156 CLAPMAKALHDAFGIQGLMTTHATGDMILDGRRGDIARRAGAAATVYPSNTGAA 215
XX 268 CLAPMAKALHDAFGIQGLMTTHATGDMILDGRRGDIARRAGAAATVYPSNTGAA 327
XX
XX 216 KALGVITPELNGKLDGAAGQVPPVGSVTELVTLDDKNVSYDEINAAKKAANDSGTYE 275
XX 328 KALGVITPELNGKLDGAAGQVPPVGSVTELVTLDDKNVSYDEINAAKKAANDSGTYE 387
XX
XX 276 DPLVSSDIIVGYSGLPDAQTQKMEVDGSLVAVVSWVDNENSTAAQVLTLEYAKIA 335
XX 388 DPLVSSDIIVGYSGLPDAQTQKMEVDGSLVAVVSWVDNENSTAAQVLTLEYAKIA 447
XX
XX 336 K 336

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DB 448 K 448
XX
XX RESULT 9
XX AAM50667
XX ID AAM50667 standard; protein, 336 AA.
XX
XX AAM50667;
XX
XX 08-APR-2002 (first entry)
XX
XX Streptococcus uberis gapC plasmin binding protein UderGapC.
XX
XX UderGapC; GapC; plasmin binding protein; epitope; infection; vaccine;
XX immunisation; mastitis; therapy.
XX
XX Streptococcus uberis.
XX
XX MO200196379-A2.
XX
XX 20-DEC-2001.
XX
XX 11-JUN-2001; 2001MO-CA000836.
XX
XX 12-JUN-2000; 2000US-0211247P.
XX
XX (UTSA-) UNIV SASKATCHEWAN.
XX
XX Potter AA, Perez-Casal J, Fontaine M;
XX
XX WPI; 2002-098051/13.
XX
XX N-ESDB; ABA91330.
XX
XX Novel GapC multiple epitope fusion polypeptide comprising antigenic
XX determinant of Streptococcus dysgalactiae, S. agalactiae, S.
XX parvuberis, or S. iniae GapC protein useful for treating mastitis in
XX vertebrates.
XX
XX Claim 8; Fig 3A-B; 116pp; English.
XX
XX The present sequence is that of the GapC plasmin binding protein,
XX UderGapC, of Streptococcus uberis ATCC 9927. The invention relates to
XX novel GapC multiple epitope fusion proteins that comprise epitopes from 1
XX or more of Streptococcus dysgalactiae, Streptococcus agalactiae,
XX Streptococcus parvuberis, Streptococcus uberis and Streptococcus iniae
XX (see AAM50665-69). A claimed example is PolyGap4 (see AAM50664).
XX Expression vectors and host cells for production of the multiple epitope
XX fusion proteins are provided. The multiple epitope proteins are used in
XX claimed vaccines for treating or preventing a bacterial infection in a
XX vertebrate, especially a streptococcal infection, and particularly
XX mastitis. They are also used in claimed methods of detecting
XX Streptococcus antibodies. The multiple epitope proteins are capable of
XX eliciting broad immunity against a variety of streptococcal infections
XX while minimizing the number of antigens present in the final formulation
XX and concomitantly reducing production costs
XX
XX SQ
XX
XX Query Match 94.3%; Score 1618; DB 5; Length 336;
XX Best Local Similarity 92.9%; Pred. No. 4,1e-136;
XX Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
XX
XX 1 MYVKVINGFGRIQLAFRRIONVEGVEVTRINDLDPNMLAHLYKDTTQGRFGTVEV 60
XX 1 MYVKVINGFGRIQLAFRRIONVEGVEVTRINDLDPNMLAHLYKDTTQGRFGTVEV 60
XX
XX 61 KEGGEVNGNFIVSAERDPE----- 120
XX 61 KEGGEVNGNFIVSAERDPE----- 120
XX
XX 61 KEGGEVNGNFIVSAERDPE----- 120
XX 61 KEGGEVNGNFIVSAERDPE----- 120
XX
XX 121 TAPGNDVKTIVFNTNHDIIIDGTEVIGASCTTNCLAPMAKALHDAFGIQGLMTTHA 180
XX
XX

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Db 121 TAPGGDVKTVFNTNHHLLDGETVTSASCTTNCCLAPMAKALQDNFVGKGLMTTTHA 180
 QY 181 YTGDDMIIDGPHRGDGLRRARAGANIVPNSGAAKALGIVTPELNGKLDGAAGRPVPT 240
 Db 181 YTGDDMIIDGPHRGDGLRRARAGANIVPNSGAAKALGIVTPELNGKLDGAAGRPVPT 240
 QY 241 GSVTELVVTLDRNVSVDENIAAMKAASNDSPGYEDPVISSDIIVSGSLFPAOTQKYM 300
 Db 241 GSVTELVVTLDRNVSVDENIAAMKAASNDSPGYEDPVISSDIIVSGSLFPAOTQKYM 300
 QY 301 EVDGSQLVKKVSVYDNEMSYTAQLVRLTEYFAKIAK 336
 Db 301 TVDGNQLVKKVSVYDNEMSYTAQLVRLTEYFAKIAK 336

RESULT 10

AAMS0641
 ID AAMS0641 standard; protein; 336 AA.

AC AAMS0641;
 XX

DT 04-APR-2002 (first entry)
 XX

DE Streptococcus uberis gapC plasmin binding protein.
 XX

KM GapC; plasmin-binding protein; UbergapC; infection; mastitis; vaccine;
 XX diagnosis; therapy.

OS Streptococcus uberis.
 XX

PN WO200196381-A2.
 XX

PD 20-DEC-2001.
 XX

PF 11-JUN-2001; 2001WO-CA000838.
 XX

PR 12-JUN-2003; 2000US-0211022P.
 XX

FA (UYSA-) UNIV SASKATCHEWAN.
 XX

FI Bolton AJ, Perez-Casal J, Fontaine M, Potter AA;
 XX

DR WPI; 2002-130725/17.
 XX

DR N-PSDB; ABA91250.
 XX

PT Novel isolated GapC protein of *Streptococcus dysgalactiae*, *S. agalactiae*,
 PT *S. uberis*, *S. parauberis*, or *S. iniae*, useful as vaccine component for
 PT treating streptococcal infection which causes mastitis in vertebrates.
 XX

PS Claim 1(c); Fig 3A-B; 107pp; English.
 XX

CC The present sequence is that of the GapC plasmin binding protein
 CC (UbergapC) of *Streptococcus uberis* ATCC 9927, encoded by the gapC gene
 CC given in ABA91250. GapC, which has no signal sequence or membrane anchor
 CC domain, is capable of eliciting an immune response in a vertebrate. The
 CC invention provides the gapC genes and proteins of 5 *Streptococcus*
 CC species, as well as recombinant vectors, host cells and vaccine
 CC compositions comprising gapC polynucleotides or proteins. The vaccines
 CC are used to treat or prevent a bacterial infection, especially a
 CC streptococcal infection, and mastitis in particular (Claimed). GapC
 CC proteins are also used in claimed methods for detecting gapC antibodies,
 CC and to raise antibodies that are used in claimed methods for detecting
 CC gapC proteins. *S. uberis* is a common pathogen associated with mastitis in
 CC cattle, horse, sheep and goat
 XX

SQ Sequence 336 AA;
 XX

Query Match 94.3%, Score 1618; DB 5; Length 336;
 Best Local Similarity 92.9%; Pred. No. 4.1e-136;

Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVAKVGINGEGRIGLAFRRIQNVGEVETVRINDLTPNMLHLKXYTQGRFPGTVEV 60
 |||

Db 1 MVAKVGINGEGRIGLAFRRIQNVGEVETVRINDLTPNMLHLKXYTQGRFPGTVEV 60
 QY 61 KEGFEVNGNPFIVKVAERDPENIDMATDGEIVTLEATGFPAXKGAERKHLAHANGAKVVI 120
 Db 61 KEGFEVNGNPFIVKVAERDPENIDMATDGEIVTLEATGFPAXKGAERKHLAHANGAKVVI 120
 QY 121 TAPGDDVKKVFPNTNHHLLDGETVTSASCTTNCCLAPMAKALQDNFVGKGLMTTTHA 180
 Db 121 TAPGDDVKKVFPNTNHHLLDGETVTSASCTTNCCLAPMAKALQDNFVGKGLMTTTHA 180
 QY 181 YTGDDMIIDGPHRGDGLRRARAGANIVPNSGAAKALGIVTPELNGKLDGAAGRPVPT 240
 Db 181 YTGDDMIIDGPHRGDGLRRARAGANIVPNSGAAKALGIVTPELNGKLDGAAGRPVPT 240
 QY 241 GSVTELVVTLDRNVSVDENIAAMKAASNDSPGYEDPVISSDIIVSGSLFPAOTQKYM 300
 Db 241 GSVTELVVTLDRNVSVDENIAAMKAASNDSPGYEDPVISSDIIVSGSLFPAOTQKYM 300
 QY 301 EVDGSQLVKKVSVYDNEMSYTAQLVRLTEYFAKIAK 336
 Db 301 TVDGNQLVKKVSVYDNEMSYTAQLVRLTEYFAKIAK 336

RESULT 11

ABP30758
 ID ABP30758 standard; protein; 336 AA.

AC ABP30758;
 XX

DT 02-JUL-2002 (first entry)
 XX

DE Streptococcus polytypide SEQ ID NO 10692.
 XX

KM Streptococcus; GAS; GBS; group B streptococcus; *Streptococcus agalactiae*;
 KM group A streptococcus; *Streptococcus pyogenes*; antibacterial;
 KM antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX

OS Streptococcus agalactiae.
 XX

PN WO200234771-A2.
 XX

PD 02-MAY-2002.
 XX

PF 23-OCT-2001; 2001WO-GB004789.
 XX

PR 27-OCT-2000; 2000GB-00026333.
 XX

PR 24-NOV-2000; 2000GB-00028727.
 XX

PR 07-MAR-2001; 2001GB-00005640.
 XX

PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX

PI Telford J, Masigiani V, Margarit Y Rosl, Grandi G, Fraser C;
 PI Tettein H;
 XX

DR WPI; 2002-352536/38.
 XX

DR N-PSDB; ABA71389.
 XX

PT New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.
 XX

PS Claim 1; Page 4179; 4525pp; English.
 XX

CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (*Streptococcus agalactiae*) or group A streptococcus/GAS
 CC (*Streptococcus pyogenes*), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABA66044-ABA71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a

CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are useful for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins
XX
SQ Sequence 336 AA;

Query Match 93.8%; Score 1609; DB 5; Length 336;
Best Local Similarity 92.0%; Pred. No. 2,6e-135;
Matches 309; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

QY 1 M V V K G I N G F G R I G L A P R I O N V G E V T R I N D L T D P N M A H L K Y D T O G R P D G T V E V 60
DB 1 M V V K G I N G F G R I O R L A P R I O N V G E V T R I N D L T D P N M A H L K Y D T O G R P D G T V E V 60
QY 61 K E G G F E V N G F I K V S A E R P E N I D M A T D G V E I V L A T G F P A K E K A E K H L A N G A K V I 120
DB 61 K E G G F E V N G F V K V S A E R P E N I D M A T D G V E I V L A T G F P A K E K A E K H L A N G A K V I 120
QY 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
DB 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
QY 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
DB 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
QY 181 Y T G D Q M I L D G P H R G D L R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A Q R V P P T 240
DB 181 Y T G D Q M I L D G P H R G D L R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A Q R V P P T 240
QY 241 G S V T E L V T L D K N V S V D E I N A M K A A S N D S F G Y T E D P I V S S D I V G S Y G S L F D A T O F K V M 300
DB 241 G S V T E L V A T E K V V E V N A M K A A A N D S Y G T E D P I V S S D I V G S L F D A T O F K V M 300
QY 301 E V D S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T V D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 12

AA050666
ID AA050666 standard; protein; 336 AA.

AC AA050666;

DT 08-APR-2002 (first entry)

DB Streptococcus agalactiae gapC plasmin binding protein AgalGapC.

XX AgalGapC; GapC; plasmin binding protein; epitope; infection; vaccine;

KW immunisation; mastitis; therapy.

OS Streptococcus agalactiae.

XX WO200196379-A2.

XX 20-DEC-2001.

XX 11-JUN-2001; 2001WO-CA000836.

XX 12-JUN-2000; 2000US-0211247P.

XX (UTSA-) UNIV SASKATCHEWAN.

XX Potter AA, Perez-Casal J, Fontaine M;

XX MPF; 2002-098051/13.

XX N-PSDB; ABA91329.

PT Novel GapC multiple epitope fusion polypeptide comprising antigenic
ET determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, S.
ET parameters, or S. iniae GapC protein useful for treating mastitis in

PT vertebrates.

XX Claim 8; Fig 2A-B; 116pp; English.

XX The present sequence is that of the GapC plasmin binding protein.
XX AgalGapC, of Streptococcus agalactiae ATCC 27541. The invention relates
XX to novel GapC multiple epitope fusion proteins that comprise epitopes
XX from 1 or more of Streptococcus dysgalactiae, Streptococcus agalactiae,
XX Streptococcus parvubertis, Streptococcus uberis and Streptococcus iniae
XX (see AA050665-69). A claimed example is PolyGap4 (see AA050664).
XX Expression vectors and host cells for production of the multiple epitope
XX fusion proteins are provided. The multiple epitope proteins are used in
XX claimed vaccines for treating or preventing a bacterial infection in a
XX vertebrate, especially a streptococcal infection, and particularly
XX mastitis. They are also used in claimed methods of detecting
XX Streptococcus antibodies. The multiple epitope proteins are capable of
XX eliciting broad immunity against a variety of streptococcal infections
XX while minimizing the number of antigens present in the final formulation
XX and concomitantly reducing production costs

SQ Sequence 336 AA;

Query Match 93.4%; Score 1602; DB 5; Length 336;
Best Local Similarity 91.7%; Pred. No. 1.1e-134;
Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 M V V K G I N G F G R I G L A P R I O N V G E V T R I N D L T D P N M A H L K Y D T O G R P D G T V E V 60
DB 1 M V V K G I N G F G R I O R L A P R I O N V G E V T R I N D L T D P N M A H L K Y D T O G R P D G T V E V 60
QY 61 K E G G F E V N G F I K V S A E R P E N I D M A T D G V E I V L A T G F P A K E K A E K H L A N G A K V I 120
DB 61 K E G G F E V N G F V K V S A E R P E N I D M A T D G V E I V L A T G F P A K E K A E K H L A N G A K V I 120
QY 61 K E G G F E V N G F V K V S A E R P E N I D M A T D G V E I V L A T G F P A K E K A E K H L A N G A K V I 120
DB 61 K E G G F E V N G F V K V S A E R P E N I D M A T D G V E I V L A T G F P A K E K A E K H L A N G A K V I 120
QY 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
DB 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
QY 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
DB 121 T A P G N D V K V T V E N T H D I L D G T E V I S G A S C T T N C L A P A K A L H D A F G I O K G M T T I H A 180
QY 181 Y T G D Q M I L D G P H R G D L R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A Q R V P P T 240
DB 181 Y T G D Q M I L D G P H R G D L R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A Q R V P P T 240
QY 241 G S V T E L V T L D K N V S V D E I N A M K A A S N D S F G Y T E D P I V S S D I V G S Y G S L F D A T O F K V M 300
DB 241 G S V T E L V A T E K V V E V N A M K A A A N D S Y G T E D P I V S S D I V G S L F D A T O F K V M 300
QY 301 E V D S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T V D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 13

AA050640
ID AA050640 standard; protein; 336 AA.

AC AA050640;

DT 04-APR-2002 (first entry)

DB Streptococcus agalactiae gapC plasmin binding protein.

XX GapC; plasmin-binding protein; AgalGapC; infection; mastitis; vaccine;

KW diagnosis; therapy.

OS Streptococcus agalactiae.

XX WO200196381-A2.

XX 20-DEC-2001.

XX 11-JUN-2001; 2001WO-CA000838.

XX 12-JUN-2000; 2000US-0211022P.

XX (UTSA-) UNIV SASKATCHEWAN.
 PA Bolton AJ, Perez-Casal J, Fontaine M, Potter AA;
 PI
 XX
 DR WPI: 2002-130725/17.
 DR N-PSDB; ABX91249.
 XX
 XX Novel isolated GapC protein of *Streptococcus dysgalactiae*, *S. agalactiae*,
 PT *S. uberis*, *S. parvubertis*, or *S. infantiae*, useful as vaccine component for
 PT treating streptococcal infection which causes mastitis in vertebrates.
 XX
 PS Claim 1 (b); Fig 2A-B; 107pp; English.
 XX
 XX The present sequence is that of the GapC plasmid binding protein
 CC (AgalGapC) of *Streptococcus agalactiae* ATCC 27541, encoded by the GapC
 CC gene given in ABA91249. GapC, which has no signal sequence or membrane
 CC anchor domain, is capable of eliciting an immune response in a
 CC vertebrate. The invention provides the GapC genes and proteins of 5
 CC *Streptococcus* species, as well as recombinant vectors, host cells and
 CC vaccine compositions comprising GapC polynucleotides or proteins. The
 CC vaccines are used to treat or prevent a bacterial infection, especially a
 CC streptococcal infection, and mastitis in particular (claimed). GapC
 CC proteins are also used in claimed methods for detecting GapC antibodies,
 CC and to raise antibodies that are used in claimed methods for detecting
 CC GapC proteins. *S. agalactiae* is a common pathogen associated with
 CC mastitis in cattle, horse, sheep and goat. It also causes septicemia,
 CC meningitis, bacteraemia, impetigo, arthritis, urinary tract infections,
 CC abscesses, spontaneous abortion, etc
 CC
 XX Sequence 336 AA:
 SQ
 Query Match 93.4%; Score 1602; DB 5; Length 336;
 Best Local Similarity 91.7%; Pred. No. 1,1e-134;
 Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 MMYVVGINGRIGRLAERFRIQNVGEVTRINDLIDPMALHLKXDTTQREPGTVEV 60
 DB 1 MMYVVGINGRIGRLAERFRIQNVGEVTRINDLIDPMALHLKXDTTQREPGTVEV 60
 QY 61 KEGGFVNGKFIKVAERDPENIDMATDGEIVLEATGFPAKKEAAEKHLAHNAGKXVYI 120
 DB 61 KEGGFVNGKFIKVAERDPENIDMATDGEIVLEATGFPAKKEAAEKHLAHNAGKXVYI 120
 QY 121 TAPGNDVKTVEVNNHDLDTETVYISGASCTTNCAPAKAHLDAFGIQLGMLTTTHA 180
 DB 121 TAPGNDVKTVEVNNHDLDTETVYISGASCTTNCAPAKAHLDAFGIQLGMLTTTHA 180
 QY 181 YTGDDMLIDGPHRGSPLRRARAGANIVPNSGAAGAIGLYIPELNKLIDGAARVPVPT 240
 DB 181 YTGDDMLIDGPHRGSPLRRARAGANIVPNSGAAGAIGLYIPELNKLIDGAARVPVPT 240
 QY 241 GSVEIVLVTLEKQVTEVEFNAMKAAANDSGVTEDEPIVSDIVGISGLFDAQTVQ 300
 DB 241 GSVEIVLVTLEKQVTEVEFNAMKAAANDSGVTEDEPIVSDIVGISGLFDAQTVQ 300
 QY 301 EYDGSQIVKVSQWIDNKSQYTLQVRLTEPAKIAK 336
 DB 301 EYDGSQIVKVSQWIDNKSQYTLQVRLTEPAKIAK 336
 QY 301 TVDGNQIVKVSQWIDNKSQYTLQVRLTEPAKIAK 336
 DB 301 TVDGNQIVKVSQWIDNKSQYTLQVRLTEPAKIAK 336

RESULT 14
 AB002516
 ID AB002516 standard; protein; 335 AA.
 XX
 AC AB002516;
 XX
 DT 23-OCT-2003 (revised)
 DT 11-FEB-2003 (first entry)
 XX
 DE S. pneumoniae type 4 strain protein from coding region #2094.
 XX
 KV Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;

KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
 KW gene therapy; vaccine.
 XX
 XX *Streptococcus pneumoniae*, type 4 strain.
 OS
 XX WO200277021-A2.
 PN
 XX
 PD 03-OCT-2002.
 XX
 PF 27-MAR-2002; 2002MO-IB002163.
 XX
 PR 27-MAR-2001; 2001GB-00007658.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 PI Masignani V, Tettelin H, Fraser C;
 XX
 DR WPI: 2003-040579/03.
 DR N-PSDB; ABX07806.
 XX
 PT New proteins and nucleic acid molecules from *Streptococcus pneumoniae*,
 PT useful as medicaments for treating or preventing a disease or infection
 PT due to *Streptococcus* bacteria, such as pneumonia, sepsis, otitis media or
 PT ear infection.
 XX
 PS Claim 1; SEQ ID NO 4189; 56pp; English.
 XX
 XX The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identified DNA coding regions from the
 CC *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as
 CC AB554544. Also included are an antibody which binds one of the proteins,
 CC treating a patient by administering the protein, DNA or antibody (in a
 CC composition), a kit comprising first and second primers, which are the
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a
 CC sequence not defined in the specification, for amplifying a target
 CC sequence contained within a *Streptococcus* nucleic acid sequence, where
 CC the first primer is substantially complementary to the target sequence
 CC and the second primer is substantially complementary to the complement of
 CC the target sequence, and where the parts of the primers having
 CC substantial complementarity define the termini of the target sequence to
 CC be amplified, assay comprising contacting a test compound with the
 CC protein, and determining whether the test compound binds to the protein
 CC and a *Streptococcus pneumoniae* bacterium, where one or more genes
 CC encoding the protein has been rendered inactive. The proteins, nucleic
 CC acid molecules, antibody and compositions are useful as medicaments for
 CC treating or preventing a disease or infection due to *Streptococcus*
 CC bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis
 CC media or ear infection. They are also useful in developing vaccines,
 CC diagnostics and antibiotics. The methods are useful for identifying
 CC immunodominant proteins. The present sequence is one of the 2469 proteins
 CC expressed by the identified coding regions from the genomic sequence.
 CC Note: The sequence data for this patent did not form part of the printed
 CC at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 335 AA:
 Query Match 92.9%; Score 1593.5; DB 6; Length 335;
 Best Local Similarity 92.6%; Pred. No. 6.3e-134;
 Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 MMYVVGINGRIGRLAERFRIQNVGEVTRINDLIDPMALHLKXDTTQREPGTVEV 60
 DB 1 MMYVVGINGRIGRLAERFRIQNVGEVTRINDLIDPMALHLKXDTTQREPGTVEV 60
 QY 61 KEGGFVNGKFIKVAERDPENIDMATDGEIVLEATGFPAKKEAAEKHLAHNAGKXVYI 120
 DB 61 KEGGFVNGKFIKVAERDPENIDMATDGEIVLEATGFPAKKEAAEKHLAHNAGKXVYI 120

CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 359 AA;

Query Match
 Best Local Similarity 92.9%; Score 1593.5; DB 4; Length 359;
 Best Local Similarity 92.6%; Pred. No. 6.9e-134;
 Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 MYKVGINGFGRIQLAFRIQVGVETVRINDLTPMMLAHLLKYDTTGRFDGTEV 60
 DB 25 MYKVGINGFGRIQLAFRIQVGVETVRINDLTPMMLAHLLKYDTTGRFDGTEV 84
 QY 61 KEGFEVNGNFKVSAERDPENIDMTGVEIVLEATGFAKKEAEGLHANKKVVY 120
 DB 85 KEGFEVNGNFKVSAERDPENIDMTGVEIVLEATGFAKKEAEGLHANKKVVY 143
 QY 121 TAPGNDVKTIVFNTNHDILDGTEYVTSASCTTNCCLAPAKALHDAFGIOKGMTTHA 180
 DB 144 TAPGNDVKTIVFNTNHDILDGTEYVTSASCTTNCCLAPAKALHDAFGIOKGMTTHA 203
 QY 161 YTGQMTLDGPHRGDLRRARAGANIVPNSGAKAIGVITPELNGKLDGSAORVPPT 240
 DB 204 YTGQMTLDGPHRGDLRRARAGANIVPNSGAKAIGVITPELNGKLDGSAORVPPT 263
 QY 241 GSVTELVVTLDDKNVSYDEINAMKAASNDSPGYTDPVSSDIYGVSYSLPDATQTKM 300
 DB 264 GSVTELVVTLDDKNVSYDEINAMKAASNDSPGYTDPVSSDIYGVSYSLPDATQTKM 323
 QY 301 EVDGSOLVKVSWYDNEMSYTAQLVRLTEYFAKIAK 336
 DB 324 DVDGKQLVKVVSWYDNEMSYTAQLVRLTEYFAKIAK 359

RESULT 15
 AAU37576
 ID AAU37576 standard; protein; 359 AA.
 XX
 AC AAU37576;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Streptococcus pneumoniae cellular proliferation protein #5.
 XX
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 XX antibacterial; drug design.
 XX
 OS Streptococcus pneumoniae.
 XX
 EN MO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242576P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (BLIT-) EUTRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind TW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 DR N-PDB; AAS55435.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 13169; 511bp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic

Search completed: May 5, 2004, 14:19:41
 Job time : 60 secs

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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:18:39 ; Search time 23 Seconds

(Without alignments)
754.188 Million cell updates/sec

Title: US-09-878-781-4

Perfect score: 1715

Sequence: 1 MYVKGINGGRIGRLAFRR.....EMSYAQLVRLTEFFAKIAK 336

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgm2_6/ptodata/2/1aa/5A COMB pep:*
2: /cgm2_6/ptodata/2/1aa/5B COMB pep:*
3: /cgm2_6/ptodata/2/1aa/6A COMB pep:*
4: /cgm2_6/ptodata/2/1aa/6B COMB pep:*
5: /cgm2_6/ptodata/2/1aa/6C COMB pep:*
6: /cgm2_6/ptodata/2/1aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1715	100.0	336	4	US-09-878-766A-12
2	1711	99.8	336	1	US-07-928-462-2
3	1711	99.8	336	3	US-08-273-247-2
4	1656.5	96.6	448	4	US-09-878-766A-22
5	1618	94.3	336	4	US-09-878-766A-16
6	1602	93.4	336	4	US-09-878-766A-14
7	1584	92.4	336	4	US-09-878-766A-20
8	1578	92.0	336	4	US-09-878-766A-18
9	1549.5	90.3	333	3	US-08-961-083-54
10	1549.5	90.3	333	4	US-09-536-784-54
11	1337.5	79.0	346	4	US-09-134-000C-4400
12	1335.5	77.3	333	4	US-09-107-532A-4769
13	1190	69.4	348	4	US-09-134-001C-5513
14	967	56.4	357	4	US-09-134-000C-4229
15	966	56.3	349	4	US-09-634-238-233
16	959	55.9	349	4	US-09-489-039A-13939
17	896.5	52.3	335	6	5290690-9
18	885.5	51.6	334	6	5290690-10
19	835.5	48.7	334	6	5290690-11
20	830	48.4	335	4	US-09-489-039A-7679
21	824.5	48.1	340	3	US-09-095-855-205
22	824.5	48.1	340	4	US-09-205-426-205
23	799	46.6	340	4	US-09-543-681A-8083
24	770.5	44.9	352	4	US-09-489-039A-9410
25	766.5	44.7	282	4	US-09-107-532A-4057
26	740.5	43.2	336	4	US-09-198-452A-662
27	736	42.9	338	4	US-09-091-725-10

28	718.5	41.9	335	2	US-08-903-800A-6	Sequence 6, Appl
29	715	41.7	340	4	US-09-252-991A-21612	Sequence 21612, A
30	709.5	41.4	334	4	US-09-674-826B-6	Sequence 6, Appl
31	699.5	40.8	268	2	US-08-997-080-186	Sequence 186, App
32	699.5	40.8	268	2	US-08-997-362-186	Sequence 186, App
33	699.5	40.8	268	3	US-09-095-855-186	Sequence 186, App
34	699.5	40.8	268	4	US-09-324-542-186	Sequence 186, App
35	699.5	40.8	268	4	US-09-205-426-186	Sequence 186, App
36	697.5	40.7	341	4	US-09-134-001C-3783	Sequence 3783, App
37	667.5	38.9	333	3	US-09-532-803-11	Sequence 11, Appl
38	659.5	38.5	333	3	US-09-532-803-9	Sequence 9, Appl
39	645	37.6	277	4	US-09-548-938A-13	Sequence 13, Appl
40	580	33.8	350	4	US-09-489-039A-11854	Sequence 11854, A
41	572.5	33.4	340	4	US-09-328-352-6704	Sequence 6704, Ap
42	570	33.2	442	4	US-09-540-236-3378	Sequence 3378, Ap
43	553	32.2	417	4	US-09-540-236-3470	Sequence 3470, Ap
44	552	32.2	359	4	US-09-543-681A-6082	Sequence 6082, Ap
45	549	32.0	367	4	US-09-252-991A-19846	Sequence 19846, A

ALIGNMENTS

RESULT 1	US-09-878-766A-12	Application US/09878766A
Sequence 12, Appl	US-09-878-766A-12	Patent No. 6660270
GENERAL INFORMATION:		
APPLICANT: Potter, Andrew A.		
APPLICANT: Perez-Casal, Jose		
APPLICANT: Fontaine, Michael		
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GABC PROTEIN		
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION		
FILE REFERENCE: 9900-0057		
CURRENT APPLICATION NUMBER: US/09/878, 766A		
CURRENT FILING DATE: 2001-09-10		
NUMBER OF SEQ ID NOS: 22		
SOFTWARE: PatentIn Ver. 2.0		
SEQ ID NO 12		
LENGTH: 336		
TYPE: PRT		
ORGANISM: Streptococcus dysgalactiae		
US-09-878-766A-12		
Query Match	100.0%; Score 1715; DB 4; Length 336;	
Best Local Similarity	100.0%; Pred. No. 4.2e-164;	
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MYVKGINGGRIGRLAFRRIONVEGYEVRINDLTPNNLAHLKDTTQGRPGTYEV 60	
DB	1 MYVKGINGGRIGRLAFRRIONVEGYEVRINDLTPNNLAHLKDTTQGRPGTYEV 60	
QY	61 KEGGEVNGPITVSERDPENIDMTDGEIVLEATGEPFAKKEAKKHLHANGAKKVI 120	
DB	61 KEGGEVNGPITVSERDPENIDMTDGEIVLEATGEPFAKKEAKKHLHANGAKKVI 120	
QY	121 TARGNDKIVTNTNHDLDGTETVIGSACTTNCALPMKALHDAFQIGKMTTTHA 180	
DB	121 TARGNDKIVTNTNHDLDGTETVIGSACTTNCALPMKALHDAFQIGKMTTTHA 180	
QY	181 YTGDMILIDPHRGGLRARRAGAAIVPNSGAAGVITPELNKLDGAORPVPT 240	
DB	181 YTGDMILIDPHRGGLRARRAGAAIVPNSGAAGVITPELNKLDGAORPVPT 240	
QY	241 GSVELVYTLDSKVSDEINAMKAASNDSPGYTBDPIVSSDIVGSGLFDATQTKM 300	
DB	241 GSVELVYTLDSKVSDEINAMKAASNDSPGYTBDPIVSSDIVGSGLFDATQTKM 300	
QY	301 EVDGSQIVKVSVDNENSTQAQLVRLTEFFAKIAK 336	
DB	301 EVDGSQIVKVSVDNENSTQAQLVRLTEFFAKIAK 336	

RESULT 2

US-07-928-462-2
Sequence 2, Application US/07928462
Patent No. 5328996
GENERAL INFORMATION:
APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: von Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmid Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,462
FILING DATE: 19920810
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
APPLICATION NUMBER: US 07/330,849
PRIOR APPLICATION DATA:
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-13.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-928-462-2

Query Match 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1,1e-163; Mismatches 334; Conservative 2; Indels 0; Gaps 0;

QY 1 MVTGKINGRGRIGR.AFRRIQNVGVYTRINDLDPNMLAHILKDTTQGRFGTVEV 60
DB 1 MVTGKINGRGRIGR.AFRRIQNVGVYTRINDLDPNMLAHILKDTTQGRFGTVEV 60
QY 61 KEGGFVNQNFIKYSAERDPENIDMTDGVETLVEATGFPKKEAAEGLHANGAKKVI 120
DB 61 KEGGFVNQNFIKYSAERDPENIDMTDGVETLVEATGFPKKEAAEGLHANGAKKVI 120
QY 121 TAPGNDVKTIVNINHDLIDGTEVTSASCTTNCLAPMAKALHDAFGIOKGLMTTTHA 180
DB 121 TAPGNDVKTIVNINHDLIDGTEVTSASCTTNCLAPMAKALHDAFGIOKGLMTTTHA 180
QY 181 YTGDMILIDGPHRGGLRRARAGANIVPNSTGAAGAIGLVIPELNGLDGAAGRVPPT 240
DB 181 YTGDMILIDGPHRGGLRRARAGANIVPNSTGAAGAIGLVIPELNGLDGAAGRVPPT 240
QY 241 GSVTELVVTLIDKRVYDELSNMAKASNDSTFGTTELPVSSDIYGVSGSLPDATQTVM 300
DB 241 GSVTELVVTLIDKRVYDELSNMAKASNDSTFGTTELPVSSDIYGVSGSLPDATQTVM 300

QY 301 EVDGSQLVYVSWYDNEMSYTAQVLTLEYPAKTAK 336
DB 301 EVDGSQLVYVSWYDNEMSYTAQVLTLEYPAKTAK 336

RESULT 3

US-08-273-247-2
Sequence 2, Application US/08273247
Patent No. 6136323
GENERAL INFORMATION:
APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: von Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmid Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,247
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
APPLICATION NUMBER: US 07/330,849
PRIOR APPLICATION DATA:
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF/S&S-13.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-247-2

Query Match 99.8%; Score 1711; DB 3; Length 336;

Best Local Similarity 99.4%; Pred. No. 1,1e-163; Mismatches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTGKINGRGRIGR.AFRRIQNVGVYTRINDLDPNMLAHILKDTTQGRFGTVEV 60
DB 1 MVTGKINGRGRIGR.AFRRIQNVGVYTRINDLDPNMLAHILKDTTQGRFGTVEV 60
QY 61 KEGGFVNQNFIKYSAERDPENIDMTDGVETLVEATGFPKKEAAEGLHANGAKKVI 120
DB 61 KEGGFVNQNFIKYSAERDPENIDMTDGVETLVEATGFPKKEAAEGLHANGAKKVI 120
QY 121 TAPGNDVKTIVNINHDLIDGTEVTSASCTTNCLAPMAKALHDAFGIOKGLMTTTHA 180
DB 121 TAPGNDVKTIVNINHDLIDGTEVTSASCTTNCLAPMAKALHDAFGIOKGLMTTTHA 180
QY 181 YTGDMILIDGPHRGGLRRARAGANIVPNSTGAAGAIGLVIPELNGLDGAAGRVPPT 240
DB 181 YTGDMILIDGPHRGGLRRARAGANIVPNSTGAAGAIGLVIPELNGLDGAAGRVPPT 240

QY 241 GSVTELVTLDRKVSVDENAMKAASNDSPGTEEDPIVSDIVSGSLFPAITQKYM 300
DB 241 GSVTELVTLDRKVSVDENAMKAASNDSPGTEEDPIVSDIVSGSLFPAITQKYM 300
QY 301 EVDGSQLVKVSWMENMSYTAQVLTLEYPAKIAK 336
DB 301 EVDGSQLVKVSWMENMSYTAQVLTLEYPAKIAK 336

RESULT 4

US-09-878-766A-22
; Sequence 22, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GapC multiple
US-09-878-766A-22

Query Match 96.6%; Score 1656.5; DB 4; Length 448;
Best Local Similarity 73.6%; Pred. No. 5.1e-158;
Matches 335; Conservative 0; Mismatches 1; Indels 85; Gaps 1;

QY 1 MVAKVGINGRIGRLAARRIONVEGVETRIINDLIDPMMALHLKDTTQGRPGCTVEV 60
DB 23 MVAKVGINGRIGRLAARRIONVEGVETRIINDLIDPMMALHLKDTTQGRPGCTVEV 87
QY 61 KEGGEVNGNFIVKSAERPE----- 81
DB 88 KEGGEVNGNFIVKSAERPE----- 147
QY 82 -----NIDMATGCVETIYLE 95
DB 148 KPEQIDWATDVEIYLEIDGTVEVEGGEFVNGQFVKVSAEREPANIDWATDVEIYLE 207
QY 96 AIGFEPAKKEAAREKHLHANGAKKVVITAPGNDVTVVPTNNDILIDGETIVISGASCTTN 155
DB 208 AIGFEPAKKEAAREKHLHANGAKKVVITAPGNDVTVVPTNNDILIDGETIVISGASCTTN 267
QY 156 CLAPAKALHDAFGIOKGLMTTTHAYTGDQMLIDGPHRGDLRRRAAGANIVPNSGAA 215
DB 268 CLAPAKALHDAFGIOKGLMTTTHAYTGDQMLIDGPHRGDLRRRAAGANIVPNSGAA 327
QY 216 KALGVITPELNGKLDGAAGRPVPPGSTEIVTLTKNYSVDEINAMKAASNDSPGTE 275
DB 328 KALGVITPELNGKLDGAAGRPVPPGSTEIVTLTKNYSVDEINAMKAASNDSPGTE 387
QY 276 DPTVSSDIVSGSLFPAITQKVEVDSQLVKVSWMENMSYTAQVLTLEYPAKIA 335
DB 388 DPTVSSDIVSGSLFPAITQKVEVDSQLVKVSWMENMSYTAQVLTLEYPAKIA 447
QY 336 K 336
DB 448 K 448

RESULT 5
US-09-878-766A-16

; Sequence 16, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus uberis
US-09-878-766A-16

Query Match 94.3%; Score 1618; DB 4; Length 336;
Best Local Similarity 92.9%; Pred. No. 2.4e-154;
Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVAKVGINGRIGRLAARRIONVEGVETRIINDLIDPMMALHLKDTTQGRPGCTVEV 60
DB 1 MVAKVGINGRIGRLAARRIONVEGVETRIINDLIDPMMALHLKDTTQGRPGCTVEV 60
QY 61 KEGGEVNGNFIVKSAERPE----- 120
DB 61 KEGGEVNGNFIVKSAERPE----- 120
QY 121 TAPGNDVKTIVPTNNDILIDGETIVISGASCTTNCLAPAKALHDAFGIOKGLMTTTHA 180
DB 121 TAPGNDVKTIVPTNNDILIDGETIVISGASCTTNCLAPAKALHDAFGIOKGLMTTTHA 180
QY 181 YTGQMTLIDGPHRGDLRRRAAGANIVPNSGAAKALGVITPELNGKLDGAAGRPVPT 240
DB 181 YTGQMTLIDGPHRGDLRRRAAGANIVPNSGAAKALGVITPELNGKLDGAAGRPVPT 240
QY 241 GSVTELVTLDRKVSVDENAMKAASNDSPGTEEDPIVSDIVSGSLFPAITQKYM 300
DB 241 GSVTELVTLDRKVSVDENAMKAASNDSPGTEEDPIVSDIVSGSLFPAITQKYM 300
QY 301 EVDGSQLVKVSWMENMSYTAQVLTLEYPAKIAK 336
DB 301 EVDGSQLVKVSWMENMSYTAQVLTLEYPAKIAK 336

RESULT 6
US-09-878-766A-14

; Sequence 14, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-878-766A-14

Query Match 93.4%; Score 1602; DB 4; Length 336;
Best Local Similarity 91.7%; Pred. No. 9.9e-153;
Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 M V V K V G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P N M L A H L K Y D T T G R F D G T V E V 60
DB 1 M V V K V G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P N M L A H L K Y D T T G R F D G T V E V 60
QY 61 K E G G F E V N G N F I K Y S A R D P E N I D M A T D G V E I V L E A T G F P A K K E A E K H L H A N G A K K V I 120
DB 61 K E G G F E V N G N F I K Y S A R D P E N I D M A T D G V E I V L E A T G F P A K K E A E K H L H A N G A K K V I 120
QY 121 T A P G N D V K T V E N T N H D L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
DB 121 T A P G N D V K T V E N T N H D L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
QY 181 Y T G D M I L D G P H R G G D L R R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A G R V P V P T 240
DB 181 Y T G D M I L D G P H R G G D L R R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A G R V P V P T 240
QY 241 G S V T E L V A V L E K D T V E E V N A M A R A A N D S Y G T E D P I V S D I V G S L P D A T Q T K V Q 300
DB 241 G S V T E L V A V L E K D T V E E V N A M A R A A N D S Y G T E D P I V S D I V G S L P D A T Q T K V Q 300
QY 301 E V D G S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T Y D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 7
US-09-878-766A-20
Sequence 20, Application US/09878766A
Patent No. 6660270
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878, 766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 20
LENGTH: 336
TYPE: PR1
ORGANISM: Streptococcus iniiae
US-09-878-766A-20

Query Match 92.4%; Score 1584; DB 4; Length 336;
Best Local Similarity 90.5%; Pred. No. 6.4e-151;
Matches 304; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 M V V K V G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P N M L A H L K Y D T T G R F D G T V E V 60
DB 1 M V V K V G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P N M L A H L K Y D T T G R F D G T V E V 60
QY 61 K E G G F E V N G N F I K Y S A R D P E N I D M A T D G V E I V L E A T G F P A K K E A E K H L H A N G A K K V I 120
DB 61 K E G G F E V N G N F I K Y S A R D P E N I D M A T D G V E I V L E A T G F P A K K E A E K H L H A N G A K K V I 120
QY 121 T A P G N D V K T V E N T N H D L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
DB 121 T A P G N D V K T V E N T N H D L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
QY 181 Y T G D M I L D G P H R G G D L R R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A G R V P V P T 240
DB 181 Y T G D M I L D G P H R G G D L R R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A G R V P V P T 240
QY 241 G S V T E L V A V L E K D T V E E V N A M A R A A N D S Y G T E D P I V S D I V G S L P D A T Q T K V Q 300
DB 241 G S V T E L V A V L E K D T V E E V N A M A R A A N D S Y G T E D P I V S D I V G S L P D A T Q T K V Q 300
QY 301 E V D G S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T Y D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 8
US-09-878-766A-18
Sequence 18, Application US/09878766A
Patent No. 6660270
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878, 766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 336
TYPE: PR1
ORGANISM: Streptococcus parauberis
US-09-878-766A-18

Query Match 92.0%; Score 1578; DB 4; Length 336;
Best Local Similarity 90.8%; Pred. No. 2.6e-150;
Matches 305; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 M V V K V G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P N M L A H L K Y D T T G R F D G T V E V 60
DB 1 M V V K V G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P N M L A H L K Y D T T G R F D G T V E V 60
QY 61 K E G G F E V N G N F I K Y S A R D P E N I D M A T D G V E I V L E A T G F P A K K E A E K H L H A N G A K K V I 120
DB 61 K E G G F E V N G N F I K Y S A R D P E N I D M A T D G V E I V L E A T G F P A K K E A E K H L H A N G A K K V I 120
QY 121 T A P G N D V K T V E N T N H D L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
DB 121 T A P G N D V K T V E N T N H D L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
QY 181 Y T G D M I L D G P H R G G D L R R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A G R V P V P T 240
DB 181 Y T G D M I L D G P H R G G D L R R A R A G A N I V P N S T G A A K A I G V I P E L N G K L D G A A G R V P V P T 240
QY 241 G S V T E L V A V L E K D T V E E V N A M A R A A N D S Y G T E D P I V S D I V G S L P D A T Q T K V Q 300
DB 241 G S V T E L V A V L E K D T V E E V N A M A R A A N D S Y G T E D P I V S D I V G S L P D A T Q T K V Q 300
QY 301 E V D G S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T Y D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 9
US-08-961-083-54
Sequence 54, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-54

Query Match 90.3%; Score 1549.5; DB 3; Length 333;
Best Local Similarity 91.3%; Pred. No. 1.9e-147;
Matches 303; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 2 VYKVGINGFGRIGRLAFRIQNVGEVETRIINDLTPNMALHLKYDTTQGRDGTVEVK 61
DB 1 VYKVGINGFGRIGRLAFRIQNVGEVETRIINDLTPNMALHLKYDTTQGRDGTVEVK 60
QY 62 EGGFEVNGFIKVSAREDPENIDMATDGEIVLEATGFFAKKEAEKHLHANGAKKVIT 121
DB 61 EGGFEVNGFIKVSAREDPENIDMATDGEIVLEATGFFAKKEAEKHLHANGAKKVIT 119
QY 122 AFGANDVKTIVFNTNHDILDEFTVIGSCTTNCCLAPMAKALHAPGIGKMTTHAY 181
DB 120 AFGANDVKTIVFNTNHDILDEFTVIGSCTTNCCLAPMAKALHAPGIGKMTTHAY 179
QY 182 TSDQWILDGPHRGDLPBARAGANIVPNSGAAKAIIGVITPELNGKLDGAAQRPVPTG 241
DB 180 TSDQWILDGPHRGDLPBARAGANIVPNSGAAKAIIGVITPELNGKLDGAAQRPVPTG 239
QY 242 SVTELAVTLDRKNSVDEINAAKKAASNDSPGYTEDPIVSSDITGVSGYSLFDATQTKWE 301
DB 240 SVTELAVTLDRKNSVDEINAAKKAASNDSPGYTEDPIVSSDITGVSGYSLFDATQTKVD 299
QY 302 VDSGQIVKVSMTDNEMSYTAQLVRLTEYPAK 333
DB 300 VDSGQIVKVSMTDNEMSYTAQLVRLTEYPAK 331

RESULT 10
US-09-536-784-54
Sequence 54, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-536-784-54

Query Match 90.3%; Score 1549.5; DB 4; Length 333;
Best Local Similarity 91.3%; Pred. No. 1.9e-147;
Matches 303; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

QY 2 VYKVGINGFGRIGRLAFRIQNVGEVETRIINDLTPNMALHLKYDTTQGRDGTVEVK 61
DB 1 VYKVGINGFGRIGRLAFRIQNVGEVETRIINDLTPNMALHLKYDTTQGRDGTVEVK 60
QY 62 EGGFEVNGFIKVSAREDPENIDMATDGEIVLEATGFFAKKEAEKHLHANGAKKVIT 121
DB 61 EGGFEVNGFIKVSAREDPENIDMATDGEIVLEATGFFAKKEAEKHLHANGAKKVIT 119
QY 122 AFGANDVKTIVFNTNHDILDEFTVIGSCTTNCCLAPMAKALHAPGIGKMTTHAY 181
DB 120 AFGANDVKTIVFNTNHDILDEFTVIGSCTTNCCLAPMAKALHAPGIGKMTTHAY 179
QY 182 TSDQWILDGPHRGDLPBARAGANIVPNSGAAKAIIGVITPELNGKLDGAAQRPVPTG 241
DB 180 TSDQWILDGPHRGDLPBARAGANIVPNSGAAKAIIGVITPELNGKLDGAAQRPVPTG 239
QY 242 SVTELAVTLDRKNSVDEINAAKKAASNDSPGYTEDPIVSSDITGVSGYSLFDATQTKWE 301
DB 240 SVTELAVTLDRKNSVDEINAAKKAASNDSPGYTEDPIVSSDITGVSGYSLFDATQTKVD 299
QY 302 VDSGQIVKVSMTDNEMSYTAQLVRLTEYPAK 333
DB 300 VDSGQIVKVSMTDNEMSYTAQLVRLTEYPAK 331

RESULT 11
US-09-134-000C-4400
Sequence 4400, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4400
LENGTH: 346
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4400
Query Match 78.0%; Score 1337.5; DB 4; Length 346;

Best Local Similarity 78.4%; Pred. No. 4,1e-126;
Matches 262; Conservative 24; Mismatches 47; Indels 1; Gaps 1;

QY 1 MYYKXGNGFGRIGRLAFRIQNVGVETRLINDLTPMKAHLKYDTQGRFGEVEV 60
DB 14 MYYKXGNGFGRIGRLAFRIQNVGVETRLINDLTPMKAHLKYDTQGRFGEVEV 73
QY 61 KEGGEVNGFRIKVSARDPENIDMATDGEIVLEATGFPKKAABKHLHANGAKKVI 120
DB 74 HEGSFNVNGKEIKVLANRNPBELPWGELGVDTLECTGFTSSAAKHLTA-GAKKVI 132
QY 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKAHLDAFGIQKGLMTTTHA 180
DB 133 SAPGNDVPTIYVNTNHTLTGKETVTSASCTTNCIAPAKAHLDAFGVSGMTTTHA 192
QY 181 YTGDMITLDPHKGDLRRARAAGANIVPNSGAKAIGVPELNGKLDGAORVPVT 240
DB 193 YTGDMITLDPHKGDLRRARAAGANIVPNSGAKAIGVPELNGKLDGAORVPVT 252
QY 241 GSVTELVTTLDGKVSVDENINAKKAASNDGTEPIVSSDIVSVSGSLFDTATQTKM 300
DB 253 GSVTELVTTLDGKVSVDENINAKKAASNDGTEPIVSSDIVSVSGSLFDTATQTKM 312
QY 301 EVDGSQLVTVSVSWYDNEMSYTAQVLTLETFPAKI 334
DB 313 TVGDKQLVTVAVMYDNEMSYTAQVLTLETFPAKI 346

RESULT 12

US-09-107-532A-4769
Sequence 4769, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4769:

SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
HYPOTHEICAL: YES

ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium

FEATURES:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...333

SEQUENCE DESCRIPTION: SEQ ID NO: 4769:
US-09-107-532A-4769

Query Match

77.3%; Score 1325.5; DB 4; Length 333;
Best Local Similarity 77.8%; Pred. No. 6.3e-125;
Matches 260; Conservative 25; Mismatches 48; Indels 1; Gaps 1;

QY 1 MYYKXGNGFGRIGRLAFRIQNVGVETRLINDLTPMKAHLKYDTQGRFGEVEV 60
DB 1 MYYKXGNGFGRIGRLAFRIQNVGVETRLINDLTPMKAHLKYDTQGRFGEVEV 60
QY 61 KEGGEVNGFRIKVSARDPENIDMATDGEIVLEATGFPKKAABKHLHANGAKKVI 120
DB 61 HEGSFNVNGKEIKVLANRNPBELPWGELGVDTLECTGFTSSAAKHLTA-GAKKVI 119
QY 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKAHLDAFGIQKGLMTTTHA 180
DB 120 SAPGNDVPTIYVNTNHTLTGKETVTSASCTTNCIAPAKAHLDAFGVSGMTTTHA 179
QY 181 YTGDMITLDPHKGDLRRARAAGANIVPNSGAKAIGVPELNGKLDGAORVPVT 240
DB 180 YTGDMITLDPHKGDLRRARAAGANIVPNSGAKAIGVPELNGKLDGAORVPVT 239
QY 241 GSVTELVTTLDGKVSVDENINAKKAASNDGTEPIVSSDIVSVSGSLFDTATQTKM 300
DB 240 GSVTELVTTLDGKVSVDENINAKKAASNDGTEPIVSSDIVSVSGSLFDTATQTKM 299
QY 301 EVDGSQLVTVSVSWYDNEMSYTAQVLTLETFPAKI 334
DB 300 TVGDKQLVTVAVMYDNEMSYTAQVLTLETFPAKI 333

RESULT 13

US-09-134-001C-5513
Sequence 5513, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

SEQ ID NO 5513

SEQ ID NO 5513

LENGTH: 348

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5513

Query Match

69.4%; Score 1190; DB 4; Length 348;
Best Local Similarity 69.4%; Pred. No. 2.9e-111;
Matches 234; Conservative 39; Mismatches 62; Indels 2; Gaps 2;

QY 1 MYYKXGNGFGRIGRLAFRIQNVGVETRLINDLTPMKAHLKYDTQGRFGEVEV 60
DB 13 MYYKXGNGFGRIGRLAFRIQNVGVETRLINDLTPMKAHLKYDTQGRFGEVEV 72
QY 61 KEGGEVNGFRIKVSARDPENIDMATDGEIVLEATGFPKKAABKHLHANGAKKVI 120
DB 73 HEGSFNVNGKEIKVLANRNPBELPWGELGVDTLECTGFTSSAAKHLTA-GAKKVI 131
QY 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKAHLDAFGIQKGLMTTTHA 180
DB 132 SAPGNDVPTIYVNTNHTLTGKETVTSASCTTNCIAPAKAHLDAFGVSGMTTTHA 191

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QY 181 YTGDMILDSHGGDLRARRAGANIVNSTGAARAGLVIPELNGKLDGAORVPY 240
DB 192 YTGDMILDSHGGDLRARRAGANIVNSTGAARAGLVIPELNGKLDGAORVPY 251
QY 241 GSVTELVTLTK-NVSYDEINAMRAASDSFGYTEDPVSSDIVSISGLPDATQY 299
DB 252 GSITELTVLTKQVTVTDQVNSAMQASDSFGYTEDPVSSDIVSISGLPDATQY 311
QY 300 MEYDSQVYKVVSVTYDNEMSYTAQVRLTLEPAKIAK 336
DB 312 MTVDROLVYKVAWYDNEMSYTAQVRLTLEPAKIAK 348

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RESULT 14

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US-09-134-000C-4229
; Sequence 4229, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent version 3.1
; SEQ ID NO 4229
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4229

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Query Match 56.4%; Score 967; DB 4; Length 357;
Best Local Similarity 58.3%; Pred. No. 8e-89;
Matches 197; Conservative 44; Mismatches 91; Indels 6; Gaps 5;

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QY 1 MYKVGINGRIGRLAERLQNV--EGEYTRINDLTPNMLAHLYDTQGRFDETE 59
DB 22 MYKVGINGRIGRLAERLQNV--EGEYTRINDLTPNMLAHLYDTQGRFDETE 81
QY 60 VKSGEFGVNGNFIKVSARDPENIDWD--GVEIVLEATGFFAKKEAAEKHLAMNAGKY 118
DB 82 ATENGIVVDGETRYAEPBSKIPVYKENGVDYLECTFYISEKKAQHLLDA--GVKRY 140
QY 119 VITAPGNDVKTIVFNTNHDILDTETVTSASCTTNCIAPMAKALHDAFGIQGLMTTI 178
DB 141 VISAPAG--AMKTIYVNVNDTLDNDKIIISAGSCTTNCIAPMAVFLNMFGEIVGTMTTV 199
QY 179 HATYGOMILDSHGGDLRARRAGANIVNSTGAARAGLVIPELNGKLDGAORVPY 238
DB 200 HATYGOMILDSHGGDLRARRAGANIVNSTGAARAGLVIPELNGKLDGAORVPY 259
QY 239 PTCGVTELVTLTK-NVSYDEINAMRAASDSFGYTEDPVSSDIVSISGLPDATQY 296
DB 260 VDSGTELVTLTK-NVSYDEINAMRAASDSFGYTEDPVSSDIVSISGLPDATQY 319
QY 297 TKYMEVDSQVYKVVSVTYDNEMSYTAQVRLTLEPAKIAK 334
DB 320 TEVTTAGDFOLVYKVAWYDNEMSYTAQVRLTLEPAKIAK 348

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RESULT 15

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US-09-634-238-233
; Sequence 233, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Hattakala, Ilka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark N.
; APPLICANT: Dekker, James

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; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U
; CURRENT APPLICATION NUMBER: US/09/634,238
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-233

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Query Match 56.3%; Score 966; DB 4; Length 340;
Best Local Similarity 57.0%; Pred. No. 9.4e-89;
Matches 195; Conservative 48; Mismatches 89; Indels 10; Gaps 6;

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QY 1 MYKVGINGRIGRLAERLQNV--EGEYTRINDLTPNMLAHLYDTQGRFDETE 56
DB 1 MYKVGINGRIGRLAERLQNV--EGEYTRINDLTPNMLAHLYDTQGRFDETE 60
QY 57 TVEVEGGEFVNGNFIKVSARDPENIDWD--GVEIVLEATGFFAKKEAAEKHLAMNAGKY 115
DB 61 EYSATDNQIYVDGKERYAYAEQAQNIPTVNDQVYVYBCTGFTSAKESQAHLLDA--CA 119
QY 116 KRVVITAPGNDVKTIVFNTNHDILDTETVTSASCTTNCIAPMAKALHDAFGIQGLMTTI 175
DB 120 KRVVITAPGNDVKTIVFNTNHDILDTETVTSASCTTNCIAPMAKALHDAFGIQGLMTTI 178
QY 176 TTHAYTQDMILDSHGGDLRARRAGANIVNSTGAARAGLVIPELNGKLDGAORVPY 235
DB 179 TTHAYTQDMILDSHGGDLRARRAGANIVNSTGAARAGLVIPELNGKLDGAORVPY 238
QY 236 VVPTGCVTELVTLTK-NVSYDEINAMRAASDSFGYTEDPVSSDIVSISGLPDATQY 292
DB 239 VVPTGCVTELVTLTK-NVSYDEINAMRAASDSFGYTEDPVSSDIVSISGLPDATQY 296
QY 293 DATQKMEVDSQVYKVVSVTYDNEMSYTAQVRLTLEPAKIAK 334
DB 299 DPTQKMEVDSQVYKVVSVTYDNEMSYTAQVRLTLEPAKIAK 340

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Search completed: May 5, 2004, 14:22:18
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:21:14 ; Search time 48 Seconds
(without alignments)
1940.327 Million cell updates/sec

Title: US-09-878-781-4
Perfect score: 1715
Sequence: 1 MVMKVGNGRIGRLAARR.....EWSYKQVLTWTFYAKIAK 336

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1715	100.0	336	9	US-09-878-766A-12
2	1715	100.0	336	10	US-09-878-781-4
3	1715	100.0	336	12	US-10-650-369-12
4	1715	100.0	336	14	US-10-134-297-4
5	1714	99.9	336	12	US-10-282-122A-74379
6	1688.5	98.5	335	10	US-09-878-781-14
7	1688.5	96.6	448	9	US-09-878-766A-22
8	1656.5	96.6	448	12	US-10-650-369-22
9	1618	94.3	336	9	US-09-878-766A-16
10	1618	94.3	336	10	US-09-878-781-8
11	1618	94.3	336	12	US-10-650-369-16
12	1618	94.3	336	14	US-10-134-297-8
13	1611	93.9	336	10	US-09-878-781-16
14	1602	93.4	336	9	US-09-878-766A-14
15	1602	93.4	336	10	US-09-878-781-6

16	1602	93.4	336	12	US-10-650-369-14	Sequence 14, Appl
17	1602	93.4	336	14	US-10-134-297-6	Sequence 6, Appl
18	1593.5	92.9	359	9	US-09-815-242-13169	Sequence 13169, A
19	1593.5	92.9	359	12	US-10-282-122A-74186	Sequence 74186, A
20	1593.5	92.9	359	9	US-09-815-242-13593	Sequence 13593, A
21	1584	92.4	336	9	US-09-878-766A-20	Sequence 20, Appl
22	1584	92.4	336	10	US-09-878-781-12	Sequence 12, Appl
23	1584	92.4	336	12	US-10-650-369-20	Sequence 20, Appl
24	1584	92.4	336	14	US-10-134-297-12	Sequence 12, Appl
25	1579.5	92.1	337	12	US-10-282-122A-72254	Sequence 72254, A
26	1578	92.0	336	9	US-09-878-766A-18	Sequence 18, Appl
27	1578	92.0	336	10	US-09-878-781-10	Sequence 10, Appl
28	1578	92.0	336	12	US-10-650-369-18	Sequence 18, Appl
29	1578	92.0	336	14	US-10-134-297-10	Sequence 10, Appl
30	1549.5	90.3	333	9	US-09-765-272-54	Sequence 54, Appl
31	1410	82.2	336	15	US-10-369-493-18524	Sequence 18524, A
32	1338.5	78.0	337	15	US-10-369-493-18342	Sequence 18342, A
33	1337.5	78.0	333	9	US-09-815-242-10847	Sequence 10847, A
34	1337.5	78.0	333	12	US-10-282-122A-57294	Sequence 57294, A
35	1277	74.5	335	12	US-10-282-122A-53266	Sequence 53266, A
36	1262	73.6	336	12	US-10-282-122A-60492	Sequence 60492, A
37	1259.5	73.4	334	12	US-10-282-122A-51519	Sequence 51519, A
38	1217.5	71.0	335	12	US-10-282-122A-71734	Sequence 71734, A
39	1197.5	69.8	334	12	US-10-282-122A-65661	Sequence 65661, A
40	1196.5	69.8	357	12	US-10-282-122A-65001	Sequence 65001, A
41	1190	69.4	336	12	US-10-282-122A-70890	Sequence 70890, A
42	1183	69.0	336	9	US-09-815-242-5618	Sequence 5618, Ap
43	1183	69.0	336	9	US-09-815-242-12540	Sequence 12540, A
44	1183	69.0	336	12	US-10-282-122A-43997	Sequence 43997, A
45	993	57.9	333	12	US-10-282-122A-56828	Sequence 56828, A

ALIGNMENTS

RESULT 1
US-09-878-766A-12
; Sequence 12, Application US/09878766A
; Patent No. US20020044928A1
; GENERAL INFORMATION:
; APPLICANT: Poter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; PILE REFERENCE: 9600-0057
; CURRENT APPLICATION NUMBER: US/09/878, 766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus dysgalactiae
US-09-878-766A-12

Query Match 100.0%; Score 1715; DB 9; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.1e-154;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVMKVGNGRIGRLAARR.....EWSYKQVLTWTFYAKIAK 60
DB 1 MVMKVGNGRIGRLAARR.....EWSYKQVLTWTFYAKIAK 60
QY 61 KEGGEVNGNFIKVSERPDENIDMADGVIVLEATGFPAKKAERKHLNANGAKVVI 120
DB 61 KEGGEVNGNFIKVSERPDENIDMADGVIVLEATGFPAKKAERKHLNANGAKVVI 120
QY 121 TAPGNDVKVVTNTNHDITGTFVTSASCTTNCAPAKALHDFGIGKAMTTTHA 180
DB 121 TAPGNDVKVVTNTNHDITGTFVTSASCTTNCAPAKALHDFGIGKAMTTTHA 180
QY 181 YIGDQMLIDGPHGSLRARRAGAAIVPNSITGAAKAIGLVIPLNQKLDGAAQVRVPPT 240

Db 181 YTGDMILDPHGGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAARVPVPT 240
Qy 241 GSVTELVVTLIDKNVSVDEINAAKKAASNDSPGYTEDPIVSSDIIVGYSGLFDATQTKVM 300
Db 241 GSVTELVVTLIDKNVSVDEINAAKKAASNDSPGYTEDPIVSSDIIVGYSGLFDATQTKVM 300
Qy 301 EVDGSQLVKKVSWYDNEMSYTAOLVRLTEYFAKIAK 336
Db 301 EVDGSQLVKKVSWYDNEMSYTAOLVRLTEYFAKIAK 336

RESULT 2

US-09-878-781-4
Sequence 4, Application US/09878781
Publication No. US20030082781A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 336
TYPE: PRT
ORGANISM: Streptococcus dysgalactiae
US-09-878-781-4

Query Match 100.0%; Score 1715; DB 10; Length 336;
Best Local Similarity 100.0%; Pred. No. 3,1e-154;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYKVGINGGRIGRLAFRIQNVGEVTRINDLPNMALHLKYDTTQGRFDGVEV 60
Db 1 MMYKVGINGGRIGRLAFRIQNVGEVTRINDLPNMALHLKYDTTQGRFDGVEV 60
Qy 61 KEGGEVNGNFIKVSARDPENIDWATDGEIVLEATGFPAKKEAAEKHLHANGAKKVI 120
Db 61 KEGGEVNGNFIKVSARDPENIDWATDGEIVLEATGFPAKKEAAEKHLHANGAKKVI 120
Qy 121 TAPGNDVKTVEVNTNHDILDTETVIGASCTTNCIAPMAKALHDAFGIQGLMTTTHA 180
Db 121 TAPGNDVKTVEVNTNHDILDTETVIGASCTTNCIAPMAKALHDAFGIQGLMTTTHA 180
Qy 181 YTGDMILDPHGGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAARVPVPT 240
Db 181 YTGDMILDPHGGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAARVPVPT 240
Qy 241 GSVTELVVTLIDKNVSVDEINAAKKAASNDSPGYTEDPIVSSDIIVGYSGLFDATQTKVM 300
Db 241 GSVTELVVTLIDKNVSVDEINAAKKAASNDSPGYTEDPIVSSDIIVGYSGLFDATQTKVM 300
Qy 301 EVDGSQLVKKVSWYDNEMSYTAOLVRLTEYFAKIAK 336
Db 301 EVDGSQLVKKVSWYDNEMSYTAOLVRLTEYFAKIAK 336

RESULT 3

US-10-650-369-12
Sequence 12, Application US/10650369
Publication No. US20040062774A1
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
AGAINST STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/10/650,369
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US/09/878,766A
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 336
TYPE: PRT
ORGANISM: Streptococcus dysgalactiae
US-10-650-369-12

Query Match 100.0%; Score 1715; DB 12; Length 336;
Best Local Similarity 100.0%; Pred. No. 3,1e-154;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYKVGINGGRIGRLAFRIQNVGEVTRINDLPNMALHLKYDTTQGRFDGVEV 60
Db 1 MMYKVGINGGRIGRLAFRIQNVGEVTRINDLPNMALHLKYDTTQGRFDGVEV 60
Qy 61 KEGGEVNGNFIKVSARDPENIDWATDGEIVLEATGFPAKKEAAEKHLHANGAKKVI 120
Db 61 KEGGEVNGNFIKVSARDPENIDWATDGEIVLEATGFPAKKEAAEKHLHANGAKKVI 120
Qy 121 TAPGNDVKTVEVNTNHDILDTETVIGASCTTNCIAPMAKALHDAFGIQGLMTTTHA 180
Db 121 TAPGNDVKTVEVNTNHDILDTETVIGASCTTNCIAPMAKALHDAFGIQGLMTTTHA 180
Qy 181 YTGDMILDPHGGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAARVPVPT 240
Db 181 YTGDMILDPHGGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAARVPVPT 240
Qy 241 GSVTELVVTLIDKNVSVDEINAAKKAASNDSPGYTEDPIVSSDIIVGYSGLFDATQTKVM 300
Db 241 GSVTELVVTLIDKNVSVDEINAAKKAASNDSPGYTEDPIVSSDIIVGYSGLFDATQTKVM 300
Qy 301 EVDGSQLVKKVSWYDNEMSYTAOLVRLTEYFAKIAK 336
Db 301 EVDGSQLVKKVSWYDNEMSYTAOLVRLTEYFAKIAK 336

RESULT 4

US-10-134-297-4
Sequence 4, Application US/10134297
Publication No. US2003016524A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055,20
CURRENT APPLICATION NUMBER: US/10/134,297
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 336
TYPE: PRT
ORGANISM: Streptococcus dysgalactiae
US-10-134-297-4

Query Match 100.0%; Score 1715; DB 14; Length 336;
Best Local Similarity 100.0%; Pred. No. 3,1e-154;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMYKVGINGGRIGRLAFRIQNVGEVTRINDLPNMALHLKYDTTQGRFDGVEV 60
Db 1 MMYKVGINGGRIGRLAFRIQNVGEVTRINDLPNMALHLKYDTTQGRFDGVEV 60
Qy 61 KEGGEVNGNFIKVSARDPENIDWATDGEIVLEATGFPAKKEAAEKHLHANGAKKVI 120

Db 61 KEGGFEVNGNFIKVAERDPENIDMAIDGVEIVLEATGPAKKAHKLHANGAKKVI 120
Qy 121 TAPGNDVKTIVFNTNHDILDGTEIVISGASCTTNCIAPMAKALHDAFGIQRKGLMTTIIHA 180
Db 121 TAPGNDVKTIVFNTNHDILDGTEIVISGASCTTNCIAPMAKALHDAFGIQRKGLMTTIIHA 180
Qy 181 YTGDMILDGPHRGDILRRARAGANIVPNSGAAKALIGVITPELNGKLDGAQRVPPT 240
Db 181 YTGDMILDGPHRGDILRRARAGANIVPNSGAAKALIGVITPELNGKLDGAQRVPPT 240
Qy 241 GSVTELVTLIDKQVSVDEINAAKASNDSPGTEDPIVSSDIIVGVSGLFPAQTOTKVM 300
Db 241 GSVTELVTLIDKQVSVDEINAAKASNDSPGTEDPIVSSDIIVGVSGLFPAQTOTKVM 300
Qy 301 EVDSSQIVKVSWMYDNEMSYTAQIVTLEYFAKIAK 336
Db 301 EVDSSQIVKVSWMYDNEMSYTAQIVTLEYFAKIAK 336

RESULT 5

US-10-282-122A-74379
Sequence 74379, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EUTRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74379
LENGTH: 336
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-10-282-122A-74379

Query Match 99.9%; Score 1714; DB 12; Length 336;
Best Local Similarity 99.7%; Pred. No. 3.8e-154;
Matches 335; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYVVGINGRIGRLAFRRIONVEGVTRINDITDPMALHLKYDTTQSRFGCTVEV 60
Db 1 MYVVGINGRIGRLAFRRIONVEGVTRINDITDPMALHLKYDTTQSRFGCTVEV 60
Qy 61 KEGGFEVNGNFIKVAERDPENIDMAIDGVEIVLEATGPAKKAHKLHANGAKKVI 120
Db 61 KEGGFEVNGNFIKVAERDPENIDMAIDGVEIVLEATGPAKKAHKLHANGAKKVI 120
Qy 121 TAPGNDVKTIVFNTNHDILDGTEIVISGASCTTNCIAPMAKALHDAFGIQRKGLMTTIIHA 180
Db 121 TAPGNDVKTIVFNTNHDILDGTEIVISGASCTTNCIAPMAKALHDAFGIQRKGLMTTIIHA 180
Qy 181 YTGDMILDGPHRGDILRRARAGANIVPNSGAAKALIGVITPELNGKLDGAQRVPPT 240
Db 181 YTGDMILDGPHRGDILRRARAGANIVPNSGAAKALIGVITPELNGKLDGAQRVPPT 240
Qy 241 GSVTELVTLIDKQVSVDEINAAKASNDSPGTEDPIVSSDIIVGVSGLFPAQTOTKVM 300
Db 241 GSVTELVTLIDKQVSVDEINAAKASNDSPGTEDPIVSSDIIVGVSGLFPAQTOTKVM 300
Qy 301 EVDSSQIVKVSWMYDNEMSYTAQIVTLEYFAKIAK 336
Db 301 EVDSSQIVKVSWMYDNEMSYTAQIVTLEYFAKIAK 336

RESULT 6

US-09-878-781-14
Sequence 14, Application US/09878781
Publication No. US20030082781A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 335
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SpyGapC
US-09-878-781-14

Query Match 98.5%; Score 1688.5; DB 10; Length 335;
Best Local Similarity 98.8%; Pred. No. 1e-151;
Matches 332; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MYVVGINGRIGRLAFRRIONVEGVTRINDITDPMALHLKYDTTQSRFGCTVEV 60
Db 1 MYVVGINGRIGRLAFRRIONVEGVTRINDITDPMALHLKYDTTQSRFGCTVEV 60
Qy 61 KEGGFEVNGNFIKVAERDPENIDMAIDGVEIVLEATGPAKKAHKLHANGAKKVI 120
Db 61 KEGGFEVNGNFIKVAERDPENIDMAIDGVEIVLEATGPAKKAHKLHANGAKKVI 120
Qy 121 TAPGNDVKTIVFNTNHDILDGTEIVISGASCTTNCIAPMAKALHDAFGIQRKGLMTTIIHA 180
Db 121 TAPGNDVKTIVFNTNHDILDGTEIVISGASCTTNCIAPMAKALHDAFGIQRKGLMTTIIHA 180
Qy 181 YTGDMILDGPHRGDILRRARAGANIVPNSGAAKALIGVITPELNGKLDGAQRVPPT 240
Db 181 YTGDMILDGPHRGDILRRARAGANIVPNSGAAKALIGVITPELNGKLDGAQRVPPT 240
Qy 241 GSVTELVTLIDKQVSVDEINAAKASNDSPGTEDPIVSSDIIVGVSGLFPAQTOTKVM 300
Db 241 GSVTELVTLIDKQVSVDEINAAKASNDSPGTEDPIVSSDIIVGVSGLFPAQTOTKVM 300

Dh 240 GSVTELVTLIDKNVSVDEINSAMKASNDSPGYEDPIVSSDIVGSYSLPDAITQKWM 299
Qy 301 EYDGSQLVKVVSVYDKNEMSYTAQVRLTLEYFAKIAK 336
Dh 300 EYDGSQLVKVVSVYDKNEMSYTAQVRLTLEYFAKIAK 335

RESULT 7

US-09-878-766A-22

Sequence 22, Application US/09878766A

Patent No. US20020044928A1

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENGTH: 448

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Gapc multiple

OTHER INFORMATION: epitope fusion protein

US-09-878-766A-22

Query Match 96.6%; Score 1656.5; DB 9; Length 448;
Best Local Similarity 79.6%; Pred. No. 1.7e-148;
Matches 335; Conservative 0; Mismatches 1; Indels 85; Gaps 1;

Qy 1 MYVKVINGFGRIGRLAFRIQNVGVSVTRINDLTDPMALHLKYDTTQGRPDGTV 60
Dh 28 MYVKVINGFGRIGRLAFRIQNVGVSVTRINDLTDPMALHLKYDTTQGRPDGTV 87
Qy 61 KEGGFVKNFNIKVSARDEP----- 81
Dh 88 KEGGFVKNFNIKVSARDEPNDMATDGVETVLEALGVTVKDGSPDNKFIKVS 147
Qy 62 -----NIDMATDGVETVLE 95
Dh 148 KDEQIDMATDGVETVLEIDGTVEYKEGFEVNGQFVKVSAREPANIOMATDGVETVLE 207
Qy 96 ATGFPAKKAERAKHLHANGAKKVVITAPGNDVTVTVFNTNHDILDTETVISA 155
Dh 208 ATGFPAKKAERAKHLHANGAKKVVITAPGNDVTVTVFNTNHDILDTETVISA 267
Qy 156 CLAPMAKALHDAFGIOKGLMTTHAYTGDMILDGPHRGDLRRARAGANIVPSTGA 215
Dh 268 CLAPMAKALHDAFGIOKGLMTTHAYTGDMILDGPHRGDLRRARAGANIVPSTGA 327
Qy 216 KAIGVIPLENGKLDGAORVPVPTGSVTELVTLIDKNVSVDEINAAKASNDSPGY 275
Dh 328 KAIGVIPLENGKLDGAORVPVPTGSVTELVTLIDKNVSVDEINAAKASNDSPGY 387
Qy 276 DPTVSSDIVGSYSLPDAITQKWEVDGSLVSVSWYDKNEMSYTAQVRLTLEYFAKIA 335
Dh 388 DPTVSSDIVGSYSLPDAITQKWEVDGSLVSVSWYDKNEMSYTAQVRLTLEYFAKIA 447
Qy 336 K 336
Dh 448 K 448

RESULT 8

US-10-650-369-22

Sequence 22, Application US/10650369

Publication No. US20040062774A1

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/10/650,369
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US/09/878,766A
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0

RESULT 9

US-09-878-766A-16

Sequence 16, Application US/09878766A

Patent No. US20020044928A1

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENGTH: 448

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Gapc multiple

OTHER INFORMATION: epitope fusion protein

US-10-650-369-22

Query Match 96.6%; Score 1656.5; DB 12; Length 448;
Best Local Similarity 79.6%; Pred. No. 1.7e-148;
Matches 335; Conservative 0; Mismatches 1; Indels 85; Gaps 1;

Qy 1 MYVKVINGFGRIGRLAFRIQNVGVSVTRINDLTDPMALHLKYDTTQGRPDGTV 60
Dh 28 MYVKVINGFGRIGRLAFRIQNVGVSVTRINDLTDPMALHLKYDTTQGRPDGTV 87
Qy 61 KEGGFVKNFNIKVSARDEP----- 81
Dh 88 KEGGFVKNFNIKVSARDEPNDMATDGVETVLEALGVTVKDGSPDNKFIKVS 147
Qy 82 -----NIDMATDGVETVLE 95
Dh 148 KDEQIDMATDGVETVLEIDGTVEYKEGFEVNGQFVKVSAREPANIOMATDGVETVLE 207
Qy 96 ATGFPAKKAERAKHLHANGAKKVVITAPGNDVTVTVFNTNHDILDTETVISA 155
Dh 208 ATGFPAKKAERAKHLHANGAKKVVITAPGNDVTVTVFNTNHDILDTETVISA 267
Qy 156 CLAPMAKALHDAFGIOKGLMTTHAYTGDMILDGPHRGDLRRARAGANIVPSTGA 215
Dh 268 CLAPMAKALHDAFGIOKGLMTTHAYTGDMILDGPHRGDLRRARAGANIVPSTGA 327
Qy 216 KAIGVIPLENGKLDGAORVPVPTGSVTELVTLIDKNVSVDEINAAKASNDSPGY 275
Dh 328 KAIGVIPLENGKLDGAORVPVPTGSVTELVTLIDKNVSVDEINAAKASNDSPGY 387
Qy 276 DPTVSSDIVGSYSLPDAITQKWEVDGSLVSVSWYDKNEMSYTAQVRLTLEYFAKIA 335
Dh 388 DPTVSSDIVGSYSLPDAITQKWEVDGSLVSVSWYDKNEMSYTAQVRLTLEYFAKIA 447
Qy 336 K 336
Dh 448 K 448

RESULT 9

US-09-878-766A-16

Sequence 16, Application US/09878766A

Patent No. US20020044928A1

GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.

APPLICANT: Perez-Casal, Jose

APPLICANT: Fontaine, Michael

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN

TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-0057

CURRENT APPLICATION NUMBER: US/09/878,766A

CURRENT FILING DATE: 2001-09-10

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16
LENGTH: 336
TYPE: PRP
ORGANISM: Streptococcus uberis
US-09-878-766A-16

Query Match 94.3%; Score 1618; DB 9; Length 336;
Best Local Similarity 92.9%; Pred. No. 5e-145;
Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 M V V K G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P M L A H L K Y D T T O G R F D G T V E V 60
DB 1 M V V K G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P M L A H L K Y D T T O G R F D G T V E V 60
QY 61 K R G F E V N G N F I K V S A R P E N I D M A T D G V E I V L A T G F P A K G A A E K H L H A N G A K K V I 120
DB 61 K R G F E V N G N F I K V S A R P E N I D M A T D G V E I V L A T G F P A K G A A E K H L H A N G A K K V I 120
QY 121 T A P G N D V K T V F E N T N H D I L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
DB 121 T A P G N D V K T V F E N T N H D I L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
QY 181 Y T G D M I L D G P H R G D L R R A R A G A N I V P N S T G A A A I G L V T P E L N G K L D G A A G R V P P T 240
DB 181 Y T G D M I L D G P H R G D L R R A R A G A N I V P N S T G A A A I G L V T P E L N G K L D G A A G R V P P T 240
QY 241 G S Y T E L V A L E K E T S V E R I N A M K A A N D S Y G T E D P I V S S D I I G M A Y S L F D A T O T K V Q 300
DB 241 G S Y T E L V A L E K E T S V E R I N A M K A A N D S Y G T E D P I V S S D I I G M A Y S L F D A T O T K V Q 300
QY 301 E V D S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T V D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 10

US-09-878-781-8
Sequence 8, Application US/09878781
Publication No. US2003082781A1
GENERAL INFORMATION:

APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
TITLE OF INVENTION: STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 336
TYPE: PRP
ORGANISM: Streptococcus uberis
US-09-878-781-8

Query Match 94.3%; Score 1618; DB 10; Length 336;
Best Local Similarity 92.9%; Pred. No. 5e-145;
Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 M V V K G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P M L A H L K Y D T T O G R F D G T V E V 60
DB 1 M V V K G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P M L A H L K Y D T T O G R F D G T V E V 60
QY 61 K R G F E V N G N F I K V S A R P E N I D M A T D G V E I V L A T G F P A K G A A E K H L H A N G A K K V I 120
DB 61 K R G F E V N G N F I K V S A R P E N I D M A T D G V E I V L A T G F P A K G A A E K H L H A N G A K K V I 120
QY 121 T A P G N D V K T V F E N T N H D I L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
DB 121 T A P G N D V K T V F E N T N H D I L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180

QY 181 Y T G D M I L D G P H R G D L R R A R A G A N I V P N S T G A A A I G L V T P E L N G K L D G A A G R V P P T 240
DB 181 Y T G D M I L D G P H R G D L R R A R A G A N I V P N S T G A A A I G L V T P E L N G K L D G A A G R V P P T 240
QY 241 G S Y T E L V A L E K E T S V E R I N A M K A A N D S Y G T E D P I V S S D I I G M A Y S L F D A T O T K V Q 300
DB 241 G S Y T E L V A L E K E T S V E R I N A M K A A N D S Y G T E D P I V S S D I I G M A Y S L F D A T O T K V Q 300
QY 301 E V D S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T V D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 11

US-10-650-369-16
Sequence 16, Application US/10650369
Publication No. US20040062774A1
GENERAL INFORMATION:

APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/10/650,369
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US/09/878,766A
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 336
TYPE: PRP
ORGANISM: Streptococcus uberis
US-10-650-369-16

Query Match 94.3%; Score 1618; DB 12; Length 336;
Best Local Similarity 92.9%; Pred. No. 5e-145;
Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 M V V K G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P M L A H L K Y D T T O G R F D G T V E V 60
DB 1 M V V K G I N G F R I G R I A F R I O N V E G V E T R I N D L T D P M L A H L K Y D T T O G R F D G T V E V 60
QY 61 K R G F E V N G N F I K V S A R P E N I D M A T D G V E I V L A T G F P A K G A A E K H L H A N G A K K V I 120
DB 61 K R G F E V N G N F I K V S A R P E N I D M A T D G V E I V L A T G F P A K G A A E K H L H A N G A K K V I 120
QY 121 T A P G N D V K T V F E N T N H D I L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
DB 121 T A P G N D V K T V F E N T N H D I L D G T E T V I S G A S C T T N C L A P M A K A L Q D N F G V K G L M T T I H A 180
QY 181 Y T G D M I L D G P H R G D L R R A R A G A N I V P N S T G A A A I G L V T P E L N G K L D G A A G R V P P T 240
DB 181 Y T G D M I L D G P H R G D L R R A R A G A N I V P N S T G A A A I G L V T P E L N G K L D G A A G R V P P T 240
QY 241 G S Y T E L V A L E K E T S V E R I N A M K A A N D S Y G T E D P I V S S D I I G M A Y S L F D A T O T K V Q 300
DB 241 G S Y T E L V A L E K E T S V E R I N A M K A A N D S Y G T E D P I V S S D I I G M A Y S L F D A T O T K V Q 300
QY 301 E V D S Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336
DB 301 T V D G N Q L V K V S W Y D N E M S Y T A Q L V R T L E Y F A K I A K 336

RESULT 12

US-10-134-297-8
Sequence 8, Application US/10134297
Publication No. US20030165524A1
GENERAL INFORMATION:

APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael

/ APPLICANT: Potter, Andrew A.
 / TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
 / FILE REFERENCE: 9000-0055.20
 / CURRENT APPLICATION NUMBER: US/10/134.297
 / CURRENT FILING DATE: 2002-04-26
 / NUMBER OF SEQ ID NOS: 12
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 8
 / LENGTH: 336
 / TYPE: PRT
 / ORGANISM: Streptococcus uberis
 / US-10-134-297-8

Query Match 94.3%; Score 1619; DB 14; Length 336;
 Best Local Similarity 92.8%; Pred. No. 5e-145;
 Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MVTGKINGFGRIGRLAFRIQNVGEVETRIINDLTPNMLAHLLKXDTTQGRFDGTEVEY 60
 DB 1 MVTGKINGFGRIGRLAFRIQNVGEVETRIINDLTPNMLAHLLKXDTTQGRFDGTEVEY 60
 QY 61 KEGFEVKNFIVKSAERDPENIDMTDGEIVLEATGFPACKAAEKHLHANGAKKVI 120
 DB 61 KEGFEVKNFIVKSAERDPENIDMTDGEIVLEATGFPACKAAEKHLHANGAKKVI 120
 QY 121 TAPGNDVKTIVFNNHDIIDGTEIVISGASCTTNCIAPAKAKLHDAFCIOXGLMTTIIA 180
 DB 121 TAPGNDVKTIVFNNHDIIDGTEIVISGASCTTNCIAPAKAKLHDAFCIOXGLMTTIIA 180
 QY 181 YTGDMITDGFHGGDLRRARAGANIVPNSGAAKAIGLVITPELNGKLDGAAGRPVPT 240
 DB 181 YTGDMITDGFHGGDLRRARAGANIVPNSGAAKAIGLVITPELNGKLDGAAGRPVPT 240
 QY 241 GSVTELVVTLIDKNVSVDEINAMKAASNSFGYTEDPVSSDIIVGVSYSGLFDATQTKM 300
 DB 241 GSVTELVVTLIDKNVSVDEINAMKAASNSFGYTEDPVSSDIIVGVSYSGLFDATQTKM 300
 QY 301 EVDGSQLVKVVSMYDNEMSYTAQVLTLEYFAKIAK 336
 DB 301 EVDGSQLVKVVSMYDNEMSYTAQVLTLEYFAKIAK 336

RESULT 13
 US-09-878-781-16
 / Sequence 16, Application US/09878781
 / Publication No. US20030082781A1
 / GENERAL INFORMATION:
 / APPLICANT: Bolton, Alexandra J.
 / APPLICANT: Perez-Casal, Jose
 / APPLICANT: Fontaine, Michael
 / APPLICANT: Potter, Andrew A.
 / TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
 / FILE REFERENCE: 9000-0055
 / CURRENT APPLICATION NUMBER: US/09/878.781
 / CURRENT FILING DATE: 2002-09-10
 / NUMBER OF SEQ ID NOS: 18
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 16
 / LENGTH: 336
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURES:
 / OTHER INFORMATION: Description of Artificial Sequence: SeqGapC
 / US-09-878-781-16

Query Match 93.9%; Score 1611; DB 10; Length 336;
 Best Local Similarity 95.2%; Pred. No. 2.3e-144;
 Matches 320; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

1 MVTGKINGFGRIGRLAFRIQNVGEVETRIINDLTPNMLAHLLKXDTTQGRFDGTEVEY 60

DB 1 MVTGKINGFGRIGRLAFRIQNVGEVETRIINDLTPNMLAHLLKXDTTQGRFDGTEVEY 60
 QY 61 KEGFEVKNFIVKSAERDPENIDMTDGEIVLEATGFPACKAAEKHLHANGAKKVI 120
 DB 61 KEGFEVKNFIVKSAERDPENIDMTDGEIVLEATGFPACKAAEKHLHANGAKKVI 120
 QY 121 TAPGNDVKTIVFNNHDIIDGTEIVISGASCTTNCIAPAKAKLHDAFCIOXGLMTTIIA 180
 DB 121 TAPGNDVKTIVFNNHDIIDGTEIVISGASCTTNCIAPAKAKLHDAFCIOXGLMTTIIA 180
 QY 181 YTGDMITDGFHGGDLRRARAGANIVPNSGAAKAIGLVITPELNGKLDGAAGRPVPT 240
 DB 181 YTGDMITDGFHGGDLRRARAGANIVPNSGAAKAIGLVITPELNGKLDGAAGRPVPT 240
 QY 241 GSVTELVVTLIDKNVSVDEINAMKAASNSFGYTEDPVSSDIIVGVSYSGLFDATQTKM 300
 DB 241 GSVTELVVTLIDKNVSVDEINAMKAASNSFGYTEDPVSSDIIVGVSYSGLFDATQTKM 300
 QY 301 EVDGSQLVKVVSMYDNEMSYTAQVLTLEYFAKIAK 336
 DB 301 EVDGSQLVKVVSMYDNEMSYTAQVLTLEYFAKIAK 336

RESULT 14
 US-09-878-766A-14
 / Sequence 14, Application US/09878766A
 / Patent No. US20020044928A1
 / GENERAL INFORMATION:
 / APPLICANT: Potter, Andrew A.
 / APPLICANT: Perez-Casal, Jose
 / APPLICANT: Fontaine, Michael
 / TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
 / FILE REFERENCE: 9000-0057
 / CURRENT APPLICATION NUMBER: US/09/878.766A
 / CURRENT FILING DATE: 2001-09-10
 / NUMBER OF SEQ ID NOS: 22
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 14
 / LENGTH: 336
 / TYPE: PRT
 / ORGANISM: Streptococcus agalactiae
 / US-09-878-766A-14

Query Match 93.4%; Score 1602; DB 9; Length 336;
 Best Local Similarity 91.7%; Pred. No. 1.7e-143;
 Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 MVTGKINGFGRIGRLAFRIQNVGEVETRIINDLTPNMLAHLLKXDTTQGRFDGTEVEY 60
 DB 1 MVTGKINGFGRIGRLAFRIQNVGEVETRIINDLTPNMLAHLLKXDTTQGRFDGTEVEY 60
 QY 61 KEGFEVKNFIVKSAERDPENIDMTDGEIVLEATGFPACKAAEKHLHANGAKKVI 120
 DB 61 KEGFEVKNFIVKSAERDPENIDMTDGEIVLEATGFPACKAAEKHLHANGAKKVI 120
 QY 121 TAPGNDVKTIVFNNHDIIDGTEIVISGASCTTNCIAPAKAKLHDAFCIOXGLMTTIIA 180
 DB 121 TAPGNDVKTIVFNNHDIIDGTEIVISGASCTTNCIAPAKAKLHDAFCIOXGLMTTIIA 180
 QY 181 YTGDMITDGFHGGDLRRARAGANIVPNSGAAKAIGLVITPELNGKLDGAAGRPVPT 240
 DB 181 YTGDMITDGFHGGDLRRARAGANIVPNSGAAKAIGLVITPELNGKLDGAAGRPVPT 240
 QY 241 GSVTELVVTLIDKNVSVDEINAMKAASNSFGYTEDPVSSDIIVGVSYSGLFDATQTKM 300
 DB 241 GSVTELVVTLIDKNVSVDEINAMKAASNSFGYTEDPVSSDIIVGVSYSGLFDATQTKM 300
 QY 301 EVDGSQLVKVVSMYDNEMSYTAQVLTLEYFAKIAK 336
 DB 301 EVDGSQLVKVVSMYDNEMSYTAQVLTLEYFAKIAK 336

RESULT 15
US-09-878-781-6
; Sequence 6, Application US/09878781
; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0055
; CURRENT APPLICATION NUMBER: US/09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-878-781-6

Query Match 93.4%; Score 1602; DB 10; Length 336;
Best Local Similarity 91.7%; Pred. No. 1,7e-143;
Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

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QY 1 MYVKVINGPGRIGRLAFPRIQVGEVTRINDLTPNNLAHLKDYDTTQGRPDGVEV 60
   |||
Db 1 MYVKVINGPGRIGRLAFPRIQVGEVTRINDLTPNNLAHLKDYDTTQGRPDGVEV 60

QY 61 KEGGEVANGNFIKVSAREDPENIDATDGEIVLEATGFFAKKEAEKHLANGAKKVI 120
   |||
Db 61 KEGGEVANGNFIKVSAREDPENIDATDGEIVLEATGFFAKKEAEKHLANGAKKVI 120

QY 121 TAPGQNBKVTVENTNHDIDGETVIGSASCTTNCLAPMAKALHDAFGIOKGLMTTHA 180
   |||
Db 121 TAPGQNBKVTVENTNHDIDGETVIGSASCTTNCLAPMAKALHDAFGIOKGLMTTHA 180

QY 181 YTGDDQMLDGPBRRGDLRRARAGANIVPNTSGAARAGIVTPELNGKLDGAARVPVPT 240
   |||
Db 181 YTGDDQMLDGPBRRGDLRRARAGANIVPNTSGAARAGIVTPELNGKLDGAARVPVPT 240

QY 241 GSYTELVVTLDPKNSVDEINAAKASNDSPGYTEDPIVSDIWEVSYSGLFDATQTKYM 300
   |||
Db 241 GSYTELVVTLDPKNSVDEINAAKASNDSPGYTEDPIVSDIWEVSYSGLFDATQTKYM 300

QY 301 EVDGSQLVKKVSWYDNEMSYTAQLVRTLEFFAKIAK 336
   |||
Db 301 EVDGSQLVKKVSWYDNEMSYTAQLVRTLEFFAKIAK 336
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Search completed: May 5, 2004, 14:27:07
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comogen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 14:17:44 ; Search time 20 Seconds

(without alignments)
1616.018 Million cell updates/sec

Title: US-09-878-781-4

Perfect score: 1715

Sequence: 1 MVVKGINGEGRIGRLAFRR.....EMSYAQLVRLTEYFAKIAK 336

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1711	99.8	336	2	A42963 glyceraldehyde-3-p
2	1617	94.3	336	2	S71350 glyceraldehyde-3-p
3	1593.5	92.9	335	2	F93235 glyceraldehyde-3-p
4	1593.5	92.9	335	2	G98099 glyceraldehyde-3-p
5	1410	82.2	336	2	F86905 glyceraldehyde-3-p
6	1338.5	78.0	337	2	G86694 hypothetical prote
7	1289.5	75.2	334	2	S34254 glyceraldehyde-3-p
8	1262	73.6	336	2	AC1382 glyceraldehyde-3-p
9	1261	73.5	336	2	AD1751 glyceraldehyde-3-p
10	1259.5	73.4	334	2	C96987 glyceraldehyde-3-p
11	1197.5	69.8	334	2	B82019 glyceraldehyde-3-p
12	1184.5	69.1	334	2	E81001 glyceraldehyde-3-p
13	1183	69.0	336	2	E89850 glyceraldehyde-3-p
14	1003	58.5	338	2	T09633 glyceraldehyde-3-p
15	993	57.9	333	2	F90881 glyceraldehyde-3-p
16	993	57.9	333	2	C85737 glyceraldehyde-3-p
17	921	53.0	337	2	S73737 glyceraldehyde-3-p
18	909.5	53.0	336	2	A43260 glyceraldehyde-3-p
19	908	52.9	337	2	C64233 glyceraldehyde-3-p
20	907	52.9	349	2	F90517 glyceraldehyde-3-p
21	886.5	52.3	335	1	DB86G glyceraldehyde-3-p
22	881.5	52.0	335	1	S12896 glyceraldehyde-3-p
23	885.5	51.6	335	1	DEB8GF glyceraldehyde-3-p
24	882.5	51.5	335	1	H84094 glyceraldehyde-3-p
25	874	51.0	333	1	DEH8GT glyceraldehyde-3-p
26	863	50.3	335	2	A70407 probable glyceral
27	843	49.2	342	2	F70391 glyceraldehyde-3-p
28	842.5	49.1	336	2	T36020 glyceraldehyde-3-p
29	831	48.5	334	2	AT0262 glyceraldehyde-3-p

30	830	48.4	331	2	F82131 glyceraldehyde-3-p
31	823	48.0	330	2	E75408 glyceraldehyde-3-p
32	822	47.9	331	2	AG0711 glyceraldehyde-3-p
33	818	47.7	331	1	DEECG3 glyceraldehyde-3-p
34	818	47.7	332	2	H90939 glyceraldehyde-3-p
35	818	47.7	332	2	DB5788 glyceraldehyde-3-p
36	816	47.6	332	2	G70915 glyceraldehyde-3-p
37	815	47.5	339	2	S72763 glyceraldehyde-3-p
38	807.5	47.1	339	2	G64041 glyceraldehyde-3-p
39	799	46.6	331	1	DETNGC glyceraldehyde-3-p
40	787.5	45.9	336	2	T40235 glyceraldehyde-3-p
41	781	45.5	337	2	S54141 glyceraldehyde-3-p
42	779.5	45.5	331	1	DETNG3 glyceraldehyde-3-p
43	779.5	45.5	337	2	S40610 glyceraldehyde-3-p
44	777.5	45.3	332	2	JC4373 glyceraldehyde-3-p
45	775	45.2	344	2	B84043 glyceraldehyde-3-p

ALIGNMENTS

RESULT 1

A42963 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Streptococci
N:Alternate names: plasmin receptor
C:Species: Streptococcus sp.
C:Date: 10-Mar-1994 #sequence revision 10-Mar-1994 #text_change 03-Jun-2002
C:Accession: A42963; B42963; JH0750
R:Dotenberg, R.; Broder, C.C.; Boyle, M.D.; Kain, S.J.; Schroeder, B.L.; Curliase III, U. Bacteriol. 174, 5204-5210, 1992
U:Title: Cloning, sequence analysis, and expression in *Escherichia coli* of a streptococcal reference number: A42963; UID:92355491; PMID:1322883
A:Reference number: A42963
A:Molecule type: DNA
A:Residues: 1-336 <LOT>
A:Experimental source: group A, strain 64/14
A:Note: sequence extracted from NCBI backbone (NCBI:110308)
A:Accession: B42963
A:Molecule type: protein
A:Residues: 2-74;161-164, 'X', 166-174;187-211, 'X', 213-217 <LOT>
R:Pancholi, V.; Fischetti, V.A.
U: Exp. Med. 176, 415-426, 1992
U:Title: A major surface protein on group A streptococci is a glyceraldehyde-3-phosphat A:Reference number: JH0750; UID:92364544; PMID:1500854
A:Accession: JH0750
A:Molecule type: protein
A:Residues: 2-30, 'A', 32-40 <PM>
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: gluconeogenesis; glycolysis; homotetramer; MAD; oxido-reductase
R:152/Active site: Cys #status predicted

Query Match 99.8%; Score 1711; DB 2; Length 336;
Best Local Similarity 99.4%; Pred. No. 4.2e-116;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVVKGINGEGRIGRLAFRRIONVEGEVTRINDITDENMLAHLLKYDTTGRPGIVEV	60
DB	1	MVVKGINGEGRIGRLAFRRIONVEGEVTRINDITDENMLAHLLKYDTTGRPGIVEV	60
QY	61	KGGFEVNAFIVTSARPDENIMADGVEIVLHATGFEAKKXEAEXKHANAKKVI	120
DB	61	KGGFEVNAFIVTSARPDENIMADGVEIVLHATGFEAKKXEAEXKHANAKKVI	120
QY	121	TAPGNDVKTIVNTNHDILDTETVTSASCTTNCIAPMAKALHDAFGIOKGLMTTTHA	180
DB	121	TAPGNDVKTIVNTNHDILDTETVTSASCTTNCIAPMAKALHDAFGIOKGLMTTTHA	180
QY	181	YTGDMTILDPHSGDILRRAPAAANTVPSGAAGATVITPELNKIDGAAGVPPPT	240
DB	181	YTGDMTILDPHSGDILRRAPAAANTVPSGAAGATVITPELNKIDGAAGVPPPT	240
QY	241	GSVEIVTLDKVSVDENNAAMAAANSFGYTEDPVSSDIIVGYSGLFEDATQTKM	300
DB	241	GSVEIVTLDKVSVDENNAAMAAANSFGYTEDPVSSDIIVGYSGLFEDATQTKM	300

Db 241 GSVTELVVTLDDKNVSVCEINSAKMAKASNDSPGTEPIVSSDIYVSGSLDPDQTQKVM 300
QY 301 EVDGSQLVKVVSWTIDNEMSYTAQVRLTEYFAKIAK 336
Db 301 EVDGSQLVKVVSWTIDNEMSYTAQVRLTEYFAKIAK 336

RESULT 2

571350
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Streptococcus
C/Species: Streptococcus "equisimilis"
C/Date: 29-Jun-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
C/Accession: S71350
R/Gase, K.; Gase, A.; Schirmer, H.; Malke, H.
Eur. J. Biochem. 239, 42-51, 1996
A/Title: Cloning, sequencing and functional overexpression of the Streptococcus equisimi-
linding protein. Purification and biochemical characterization of the protein.
A/Reference number: S71350; MOID:96305364; PMID:8706717
A/Accession: S71350
A/Molecule type: DNA
A/Residues: 1-336 <GAS>
A/Cross-references: EMBL:X87788; NID:g1478268; PIDD:CA66377.1; PID:g1478269
A/Experimental source: strain H46A
C/Genetics:
A/Gene: gapC
C/Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C/Keywords: gluconogenesis; glycolysis; NAD; oxidoreductase
F.4.3.4/Region: beta-alpha-beta NAD nucleotide-binding fold
F.152/Active site: Cys #status predicted

Query Match 94.3%; Score 1617; DB 2; Length 336;
Best Local Similarity 95.5%; Pred. No. 2.5e-109;
Matches 321; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 MYYKVGINGFGRIGRLAFRIQVGEVETRIINDLTPMNAHLKXDTTQGRPDGVEV 60
Db 1 MYYKVGINGFGRIGRLAFRIQVGEVETRIINDLTPMNAHLKXDTTQGRPDGVEV 60
QY 61 KGGFEVNGNFKIVSARDPENIDMATDGVETLEATGFPFAKKEAAEKHLHANGAKKVI 120
Db 61 KGGFEVNGNFKIVSARDPENIDMATDGVETLEATGFPFAKKEAAEKHLHANGAKKVI 120
QY 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKALHDARFGIQGLMTTTHA 180
Db 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKALHDARFGIQGLMTTTHA 180
QY 181 YTGDDMTLVGPHRGDRLRRARAGANIVPNSGTGAATIGLVIPENKLDGAAQRPVPT 240
Db 181 YTGDDMTLVGPHRGDRLRRARAGANIVPNSGTGAATIGLVIPENKLDGAAQRPVPT 240
QY 241 GSVTELVVTLDDKNVSVCEINSAKMAKASNDSPGTEPIVSSDIYVSGSLDPDQTQKVM 300
Db 241 GSVTELVVTLDDKNVSVCEINSAKMAKASNDSPGTEPIVSSDIYVSGSLDPDQTQKVM 300
QY 301 EVDGSQLVKVVSWTIDNEMSYTAQVRLTEYFAKIAK 336
Db 301 EVDGSQLVKVVSWTIDNEMSYTAQVRLTEYFAKIAK 336

RESULT 3

F95235
glyceraldehyde-3-phosphate dehydrogenase [imported] - Streptococcus pneumoniae (strain T
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: F95235
R/Retelid, H.; Nelsson, K.E.; Paulsen, I.T.; Eiserich, J.A.; Read, T.D.; Peterson, S.; Heid-
cn, U.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radume, D.; Holzapfel,
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11469396
A/Accession: F95235

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-335 <CUR>
A/Cross-references: GB:A800672; PIDD:AAK76079.1; PID:g14973522; GSPDB:GN00164; TIGR:
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP2012
C/Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 92.9%; Score 1593.5; DB 2; Length 335;
Best Local Similarity 92.6%; Pred. No. 1.3e-107;
Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 MYYKVGINGFGRIGRLAFRIQVGEVETRIINDLTPMNAHLKXDTTQGRPDGVEV 60
Db 1 MYYKVGINGFGRIGRLAFRIQVGEVETRIINDLTPMNAHLKXDTTQGRPDGVEV 60
QY 61 KGGFEVNGNFKIVSARDPENIDMATDGVETLEATGFPFAKKEAAEKHLHANGAKKVI 120
Db 61 KGGFEVNGNFKIVSARDPENIDMATDGVETLEATGFPFAKKEAAEKHLHANGAKKVI 119
QY 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKALHDARFGIQGLMTTTHA 180
Db 121 TAPGNDVKTVEFNTNHDILDTETVTSASCTTNCIAPAKALHDARFGIQGLMTTTHA 179
QY 181 YTGDDMTLVGPHRGDRLRRARAGANIVPNSGTGAATIGLVIPENKLDGAAQRPVPT 240
Db 181 YTGDDMTLVGPHRGDRLRRARAGANIVPNSGTGAATIGLVIPENKLDGAAQRPVPT 239
QY 241 GSVTELVVTLDDKNVSVCEINSAKMAKASNDSPGTEPIVSSDIYVSGSLDPDQTQKVM 300
Db 241 GSVTELVVTLDDKNVSVCEINSAKMAKASNDSPGTEPIVSSDIYVSGSLDPDQTQKVM 299
QY 301 EVDGSQLVKVVSWTIDNEMSYTAQVRLTEYFAKIAK 336
Db 301 EVDGSQLVKVVSWTIDNEMSYTAQVRLTEYFAKIAK 335

RESULT 4

G98099
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [imported] -
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
C/Accession: G98099
R/Hoshino, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.;
e, R.; Teblanc, D.J.; Lee, L.N.; Iefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.;
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: G98099
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-359 <CUR>
A/Cross-references: GB:A8007317; PIDD:AAI00628.1; PID:g15459513; GSPDB:GN00174
C/Genetics:
A/Gene: gapA
C/Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C/Keywords: oxidoreductase

Query Match 92.9%; Score 1593.5; DB 2; Length 359;
Best Local Similarity 92.6%; Pred. No. 1.4e-107;
Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 MYYKVGINGFGRIGRLAFRIQVGEVETRIINDLTPMNAHLKXDTTQGRPDGVEV 60
Db 25 MYYKVGINGFGRIGRLAFRIQVGEVETRIINDLTPMNAHLKXDTTQGRPDGVEV 84
QY 61 KGGFEVNGNFKIVSARDPENIDMATDGVETLEATGFPFAKKEAAEKHLHANGAKKVI 120
Db 85 KGGFEVNGNFKIVSARDPENIDMATDGVETLEATGFPFAKKEAAEKHLHANGAKKVI 143

Db 120 APAGNDIKTIVFWNNEDDGTETVTSIGASCTTNCIAZMAKVLNDKKEGKPMTHAY 179
Cy 182 TSDQMLTSGPHRGD:RRARAGANIVPNTSGAAYAGLVIPELNGKLDGAQRVPYTG 241
Db 180 TNDQMLTSGPHRGD:RRARAGANIVPNTSGAAYAGLVIPELNGKLDGAQRVPYTG 239
Cy 242 SVTELVTYLDKNSVDEINAAKASNDSPGYTEPIYSSDIVSGYSLPDTOTKME 301
Db 240 SVTELISVLKKNVTEIEINAAKAEKESGYTEDEIYSADVIGISGLPDTITKIVD 299
Cy 302 VDGSLYKVVSVTNDKMSYTAQVLTTEYFAKIAK 336
Db 300 VDGSLYKVVSVTNDKMSYTAQVLTTEYFAKIAK 334

RESULT 8

AC1382

glyceraldehyde 3-phosphate dehydrogenase homolog gap [imported] - *Listeria monocytogenes*C:Species: *Listeria monocytogenes*

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AC1382

R:Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karsic, U.

Science 294, 849-852, 2001

A:Authors: Krefl, U.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1382

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-336 <GLA>

A:Cross-references: GB:NC_003210; PIDD:CAD00537.1; PIDD:g1411947; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: gap

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 73.6%; Score 1262; DB 2; Length 336;
Best Local Similarity 73.3%; Pred. No. 1.1e-83;
Matches 247; Conservative 33; Mismatches 55; Indels 2; Gaps 2;

Cy 1 MVTAVGNGFGRIGRLAFRIQNVGVEVTRINDLTPNMLAHLKTYTGGPFGTVEV 60
Db 1 MVTAVGNGFGRIGRLAFRIQNVGVEVTRINDLTPNMLAHLKTYTGGPFGTVEV 60
Cy 61 KEGGFVNGNFIKVSAREPDENIDATDVEIYEAATGPFAPKKAABKHLNAGAKKVI 120
Db 61 HDGFVNGNFVKKVLANRPBELPWGDIAGVIVLECTGFTTAQDAKELHKA-GAKKVI 119
Cy 121 TAPGNDVKTVEFVFNHDLIDGTETVTSIGASCTTNCIAPAKALHDAFGIOKGLMTTIIA 180
Db 120 SAPATGDKTIVVNNHETLDGTETVTSIGASCTTNCIAPAKALHDAFGIOKGLMTTIIA 179
Cy 181 YTGDMILDGPHRGD:RRARAGANIVPNTSGAAYAGLVIPELNGKLDGAQRVPYPT 240
Db 180 YTGDMITLDAHPKDFRRARAANLIPNTGAAGAIGVLPILKELDGAQRVPYPT 239
Cy 241 GSVELVYTLTKNSVDEINAAKASNDSPGYTEPIYSSDIVSGYSLPDTOTKME 299
Db 240 GSVELVYTLTKNSVDEINAAKASNDSPGYTEPIYSSDIVSGYSLPDTOTKME 299
Cy 300 MEVDSSQLYKVVSVTNDKMSYTAQVLTTEYFAKIAK 336
Db 300 LTVGDDQLYKVVSVTNDKMSYTAQVLTTEYFAKIAK 336

RESULT 9

AD1751

glyceraldehyde 3-phosphate dehydrogenase homolog gap [imported] - *Listeria innocua* (strain C)C:Species: *Listeria innocua*

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AD1751
R:Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karsic, U.

Science 294, 849-852, 2001

A:Authors: Krefl, U.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant, A.; Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AD1751

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-336 <GLA>

A:Cross-references: GB:AL592022; PIDD:CAAC97780.1; PIDD:g1415075; GSPDB:GN00178

A:Experimental source: strain Clp11262

C:Genetics:

A:Gene: gap

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 73.5%; Score 1261; DB 2; Length 336;
Best Local Similarity 73.3%; Pred. No. 1.1e-83;
Matches 247; Conservative 32; Mismatches 56; Indels 2; Gaps 2;

Cy 1 MVTAVGNGFGRIGRLAFRIQNVGVEVTRINDLTPNMLAHLKTYTGGPFGTVEV 60
Db 1 MVTAVGNGFGRIGRLAFRIQNVGVEVTRINDLTPNMLAHLKTYTGGPFGTVEV 60
Cy 61 KEGGFVNGNFIKVSAREPDENIDATDVEIYEAATGPFAPKKAABKHLNAGAKKVI 120
Db 61 HDGFVNGNFVKKVLANRPBELPWGDIAGVIVLECTGFTTAQDAKELHKA-GAKKVI 119
Cy 121 TAPGNDVKTVEFVFNHDLIDGTETVTSIGASCTTNCIAPAKALHDAFGIOKGLMTTIIA 180
Db 120 SAPATGDKTIVVNNHETLDGTETVTSIGASCTTNCIAPAKALHDAFGIOKGLMTTIIA 179
Cy 181 YTGDMILDGPHRGD:RRARAGANIVPNTSGAAYAGLVIPELNGKLDGAQRVPYPT 240
Db 180 YTGDMITLDAHPKDFRRARAANLIPNTGAAGAIGVLPILKELDGAQRVPYPT 239
Cy 241 GSVELVYTLTKNSVDEINAAKASNDSPGYTEPIYSSDIVSGYSLPDTOTKME 299
Db 240 GSVELVYTLTKNSVDEINAAKASNDSPGYTEPIYSSDIVSGYSLPDTOTKME 299
Cy 300 MEVDSSQLYKVVSVTNDKMSYTAQVLTTEYFAKIAK 336
Db 300 LTVGDDQLYKVVSVTNDKMSYTAQVLTTEYFAKIAK 336

RESULT 10

C96987

glyceraldehyde 3-phosphate dehydrogenase, gene gapC [imported] - *Clostridium acetobutylicum*C:Species: *Clostridium acetobutylicum*

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

C:Accession: C96987

R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Li, J.; Daly, M.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C96987

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-334 <KOR>

A:Cross-references: GB:AE001437; PIDD:AAK78686.1; PIDD:g15023589; GSPDB:GN00168

A:Experimental source: *Clostridium acetobutylicum* ATCC824

C:Genetics:

A:Gene: CAC0709

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 73.4%; Score 1259.5; DB 2; Length 334;
Best Local Similarity 71.9%; Pred. No. 1.6e-83;
Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

QY 2 VYKVGINGRIGRLAERRIQWVSEVTRINDITDPMNLAKYDTTQGRPDGVEVK 61
1 MAKIANGRIGRLAERRIQWVSEVTRINDITDPMNLAKYDTTQGRPDGVEVK 60
QY 62 EGGEFVNGKFIKVAEADPENIDMADGVEIVLAEAGFPFAKKEAAEKHLHANGAKKVI 121
Db 61 EGAFVNGKVEVFAEADPEKIPMDGLIGIVALECQCFPEKKEKAHVBA-CAKKVVIS 119
QY 122 AFGNDKTVVNTNHDIDGTEVTSASCTTNCLAPMAKALHARICQKGMTHAY 181
Db 120 AFGNDKTVVNTNHDIDGTEVTSASCTTNCLAPMAKALHARICQKGMTHAY 179
QY 182 TGHOMLIDPRRGDILRRARAGANIVNSTGAAKAIGIVPELAKKLIDGAAGVPEPTG 241
Db 180 TNDQNTLDPRRGDILRRARAGANIVNSTGAAKAIGIVPELAKKLIDGAAGVPEPTG 239
QY 242 SYTELIVTLDKRVSVDEINAAKASANDSPGYTDEPIVSSDIYVSGSLPDAOTKWE 301
Db 240 SYTELIVTLDKRVSVDEINAAKASANDSPGYTDEPIVSSDIYVSGSLPDAOTKWE 299
QY 302 VDSGQLVKVVSWYDNEMSTQAQVRLTEYFKIAK 336
Db 300 VDSGQLVKVVSWYDNEMSTQAQVRLTEYFKIAK 334

RESULT 11

B82019
glyceralddehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) C:MM2046 [imp
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 03-Jun-2002
C:Accession: B82019
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
J.; Holtz, S.; Jorgensen, K.; Leather, S.; Mouton, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: B82019
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <PAR>
A:Cross-references: GB:A162752; GB:A157959; NID:g7378778; PIND:CA83554.1; PID:g737902
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: MM2046
C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match 69.8%; Score 1197.5; DB 2; Length 334;
Best local similarity 70.2%; Pred. No. 4.8e-79;
Matches 233; Conservative 33; Mismatches 65; Indels 1; Gaps 1;

QY 1 MYYKVGINGRIGRLAERRIQWVSEVTRINDITDPMNLAKYDTTQGRPDGVEVK 60
Db 1 MSIKVANGRIGRLAERRIQWVSEVTRINDITDPMNLAKYDTTQGRPDGVEVK 60
QY 61 KEGGEFVNGKFIKVAEADPENIDMADGVEIVLAEAGFPFAKKEAAEKHLHANGAKKVI 120
Db 61 KDAIYVNGKFIKVAEADPENIDMADGVEIVLAEAGFPFAKKEAAEKHLHANGAKKVI 119
QY 121 TAPGNDKTVVNTNHDIDGTEVTSASCTTNCLAPMAKALHARICQKGMTHAY 180
Db 120 TAPGNDKTVVNTNHDIDGTEVTSASCTTNCLAPMAKALHARICQKGMTHAY 179
QY 181 YTGQNTLDPRRGDILRRARAGANIVNSTGAAKAIGIVPELAKKLIDGAAGVPEPTG 240
Db 180 YTGQNTLDPRRGDILRRARAGANIVNSTGAAKAIGIVPELAKKLIDGAAGVPEPTG 239
QY 241 GSYTELIVTLDKRVSVDEINAAKASANDSPGYTDEPIVSSDIYVSGSLPDAOTKWE 300
Db 240 GSYTELIVTLDKRVSVDEINAAKASANDSPGYTDEPIVSSDIYVSGSLPDAOTKWE 299
QY 301 EVDGSLVKKVSWYDNEMSTQAQVRLTEYFKIAK 332
Db 300 EVDGSLVKKVSWYDNEMSTQAQVRLTEYFKIAK 332

Db 300 TVGKQLVKTVAWYDNEMSTQAQVRLTEYFKIAK 331

RESULT 12

B81001
glyceralddehyde 3-phosphate dehydrogenase NMB2159 [imported] - *Neisseria meningitidis* (
C:Species: *Neisseria meningitidis*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: B81001
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Piazza, W.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: B81001
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <TEXT>
A:Cross-references: GB:AE002563; GB:AE002096; NID:g7227405; PIND:AAF42467.1; PID:g7227
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB2159
C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase

Query Match 69.1%; Score 1184.5; DB 2; Length 334;
Best local similarity 69.3%; Pred. No. 4.1e-78;
Matches 230; Conservative 35; Mismatches 66; Indels 1; Gaps 1;

QY 1 MYYKVGINGRIGRLAERRIQWVSEVTRINDITDPMNLAKYDTTQGRPDGVEVK 60
Db 1 MSIKVANGRIGRLAERRIQWVSEVTRINDITDPMNLAKYDTTQGRPDGVEVK 60
QY 61 KEGGEFVNGKFIKVAEADPENIDMADGVEIVLAEAGFPFAKKEAAEKHLHANGAKKVI 120
Db 61 KDAIYVNGKFIKVAEADPENIDMADGVEIVLAEAGFPFAKKEAAEKHLHANGAKKVI 119
QY 121 TAPGNDKTVVNTNHDIDGTEVTSASCTTNCLAPMAKALHARICQKGMTHAY 180
Db 120 TAPGNDKTVVNTNHDIDGTEVTSASCTTNCLAPMAKALHARICQKGMTHAY 179
QY 181 YTGQNTLDPRRGDILRRARAGANIVNSTGAAKAIGIVPELAKKLIDGAAGVPEPTG 240
Db 180 YTGQNTLDPRRGDILRRARAGANIVNSTGAAKAIGIVPELAKKLIDGAAGVPEPTG 239
QY 241 GSYTELIVTLDKRVSVDEINAAKASANDSPGYTDEPIVSSDIYVSGSLPDAOTKWE 300
Db 240 GSYTELIVTLDKRVSVDEINAAKASANDSPGYTDEPIVSSDIYVSGSLPDAOTKWE 299
QY 301 EVDGSLVKKVSWYDNEMSTQAQVRLTEYFKIAK 332
Db 300 EVDGSLVKKVSWYDNEMSTQAQVRLTEYFKIAK 331

RESULT 13

B89850
glyceralddehyde-3-phosphate dehydrogenase [imported] - *Staphylococcus aureus* (strain N31;
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89850
R:Kurita, M.; Ohta, T.; Uchiyama, T.; Baba, T.; Yuzawa, H.; Kobayashi, T.; Qui, L.; Ogi
ma, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaishi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89850
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <KUR>
A:Cross-references: GB:BA000018; PID:g13700663; PIND:BA041960.1; GSPDB:GN00149
A:Experimental source: strain N315

C:Genetics:
A:Gene: gap
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 69.0%; Score 1183; DB 2; Length 336;
Best Local Similarity 68.2%; Pred. No. 5.3e-78;
Matches 230; Conservative 43; Mismatches 62; Indels 2; Gaps 2;

QY 1 MVRKGINFGRIGRLAFLRIQNVGVVTRINDLDPNMLHLKDTTQGRFGTEV 60
DB 1 MAVKVAINGFGRIGRLAFLRIQNVGVVTRINDLDPNMLHLKDTTQGRFGTEV 60
QY 61 KEGGEPVNGNPIKYSARDEPNIDATOGVEIVLEAFNGFAKXEAKEHLNAGAKVIT 120
DB 61 VDSGFRVNGKEVKSFPEDSKLPMKINDIVVECTGRTTKDGAQHLEA-GAKKVI 119
QY 121 TAFGNDVATVFTNTNHDLDGTEVIVSAGCTTNCIAPAKALHDAPFGIOKMTTTHA 180
DB 120 SAVAAGDKTIVFTNTNHDLDGSEIVVSGACTTNSIAPAKALHDAPFGIYEGMTTTHA 179
QY 181 YTGDDNILDGPHRGDILRRARAGANIVPNTGAAKAGIIVPELNGKLDGAORVPVPT 240
DB 180 YTGDDNITDAPHRKGDILRRARAGANIVPNTGAAKAGIIVPELNGKLDGAORVPVPT 239
QY 241 GSVTEAVTLDK-NVSVDEINAAKASNDPFGTBDPIVSSDIYVSGSLPDAOTKY 299
DB 240 GSITELTYLKRQDVTVEQVNEKMSNESFGTDEIVSSDVGMVTSLEFDATQTEV 299
QY 300 MEVDSSQLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 336
DB 300 MSVGRQLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 336

RESULT 14

T09633
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Lactobacillus
C:Species: Lactobacillus delbrueckii
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T09633
R:Barany, F.; Delacourte, F.; Garel, J.R.
Microbiology 144, 905-914, 1998
A:Title: An operon coding for three glycolytic enzymes in Lactobacillus delbrueckii subsp.

A:Reference number: Z16788; MUID:98240227; PMID:9579064
A:Accession: T09633
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-338 <BNA>
A:Cross-references: EMBL:AJ000339; NID:92624189; PIDN:CAA04014.1; PID:92624191
A:Experimental source: subsp. bulgaricus, strain B107
C:Genetics:
A:Gene: gap
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: gluconeogenesis; glycolysis; oxidoreductase

Query Match 58.5%; Score 1003; DB 2; Length 338;
Best Local Similarity 58.7%; Pred. No. 5.2e-65;
Matches 199; Conservative 45; Mismatches 89; Indels 6; Gaps 3;

QY 1 MVRKGINFGRIGRLAFLRIQNVGVVTRINDLDPNMLHLKDTTQGRFGTEV 56
DB 1 MVRKGINFGRIGRLAFLRIQNVGVVTRINDLDPNMLHLKDTTQGRFGTEV 60
QY 57 TVEKGEFVNGNPIKYSARDEPNIDATOGVEIVLEAFNGFAKXEAKEHLNAG 115
DB 61 EVSALTEDSLVVDKKEVYAEPOANIIPWAKDGDVLECTGFTTSKASQAHLDH-GA 119
QY 116 KTVVITAPAGNDVKTIVFTNTNHDLDGTEVIVSAGCTTNCIAPAKALHDAPFGIOK 175
DB 120 KTVVITAPAGNDVKTIVFTNTNHDLDGTEVIVSAGCTTNCIAPAKALHDAPFGIOK 179
QY 176 TTHAVTATQVLDGPDGRGNPNRARAANENIIPHSITGAARAKIAGLVPELNGKLDGAOR 235

DB 180 TTHAVTATQVLDGPDGRGNPNRARAANENIIPHSITGAARAKIAGLVPELNGKLDGAOR 239
QY 236 VPRVGSVTELVTELDKIVSVDEINAAKASNDPFGTBDPIVSSDIYVSGSLPDAOTKY 295
DB 240 VPRVGSVTELVTELDKIVSVDEINAAKASNDPFGTBDPIVSSDIYVSGSLPDAOTKY 299
QY 296 QTKVMEVDSSQLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 334
DB 300 QTKVMEVDSSQLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 338

RESULT 15

T09081
glyceraldehyde-3-phosphate dehydrogenase C [imported] - Escherichia coli (strain 0157
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F09081
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F09081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA035445.1; PID:913361488; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: KCS022
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 57.9%; Score 993; DB 2; Length 333;
Best Local Similarity 59.3%; Pred. No. 2.7e-64;
Matches 198; Conservative 54; Mismatches 76; Indels 6; Gaps 5;

QY 4 KVGINGFGRIGRLAFLRIQNVGVVTRINDLDPNMLHLKDTTQGRFGTEV 62
DB 3 KVGINGFGRIGRLAFLRIQNVGVVTRINDLDPNMLHLKDTTQGRFGTEV 62
QY 63 GGFVNGNPIKYSARDEPNIDATOGVEIVLEAFNGFAKXEAKEHLNAGAKKVI 122
DB 63 DSLVLDKSLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 121
QY 123 FCGNDVATVFTNTNHDLDGTEVIVSAGCTTNCIAPAKALHDAPFGIOKMTTTHA 182
DB 122 FCGNDVATVFTNTNHDLDGTEVIVSAGCTTNCIAPAKALHDAPFGIOKMTTTHA 180
QY 183 GDQNTLDGPHRGDILRRARAGANIVPNTGAAKAGIIVPELNGKLDGAORVPVPT 242
DB 181 GTOSIVDGP-RGDLFASRAAENIIPHTGAARAKIAGVPELNGKLDGAORVPVPT 239
QY 243 VTELVTELDKIVSVDEINAAKASNDPFGTBDPIVSSDIYVSGSLPDAOTKY 300
DB 240 VTELVTELDKIVSVDEINAAKASNDPFGTBDPIVSSDIYVSGSLPDAOTKY 299
QY 301 EVDSSQLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 334
DB 300 AVGDQLVNVSVWYDNEMSYTAOLVTELEFPAKIAK 333

Search completed: May 5, 2004, 14:21:42
Job time: 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 14:15:03 ; Search time 17 Seconds

(without alignments)
1029.151 Million cell updates/sec

Title: US-09-878-781-4

Perfect score: 1715

Sequence: 1 MVMKXNGRIGRIARFR.....EMSYAQWRTLEYFAKAK 336

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1709	99.7	335	1	G3P_STREY
2	1705	99.4	335	1	G3P_STRE3
3	1612	94.0	335	1	G3P_STRE0
4	1338.5	78.0	337	1	G3P_LACIA
5	1289.5	75.2	334	1	G3P_CLOPA
6	1259.5	73.4	334	1	G3P_CLOAB
7	1190	69.4	336	1	G3P_STREP
8	1183	69.0	336	1	G3P_STPAK
9	1003	58.5	338	1	G3P_LACDE
10	993	57.9	333	1	G3P_ECO57
11	992	57.8	333	1	G3P_ECOLI
12	921	53.7	337	1	G3P_MYCPN
13	908.5	53.0	334	1	G3P_CORGL
14	908	52.9	337	1	G3P_MYCGB
15	891.5	52.0	334	1	G3P_BACST
16	886.5	51.7	334	1	G3P_BACME
17	880.5	51.3	334	1	G3P_BACST
18	873	50.9	332	1	G3P_THEMA
19	863	50.3	335	1	G3P_BORBU
20	843	49.2	342	1	G3P_AQUAB
21	842.5	49.1	336	1	G3P_STRCO
22	817	47.6	330	1	G3P_SALTY
23	816	47.6	339	1	G3P_MYCTU
24	815	47.5	339	1	G3P_MYCLE
25	813	47.4	330	1	G3P_ECOLI
26	807.5	47.1	339	1	G3P_HACTN
27	801	46.7	339	1	G3P_MYCAV
28	794.5	46.3	337	1	G3P_RHTRA
29	794	45.9	330	1	G3P_TRYBB
30	787.5	45.7	336	1	G3P_SCHPO
31	784.5	45.7	332	1	G3P_RALSO
32	783.5	45.7	337	1	G3P_MOMAN
33	779.5	45.5	331	1	G3P_THENA

34	779.5	45.5	337	1	G3P_CLAPU	Q00584 claviceps p
35	777.5	45.3	332	1	G3P_STRAU	Q59800 streptomyc
36	775	45.2	333	1	G3P_STRE3	P00505 streptomyc
37	772	45.0	333	1	G3P_STRE0	P43226 streptomyc
38	772	45.0	337	1	G3P2_AANSP	P58554 anabaena sp
39	771.5	45.0	337	1	G3P_COCHR	P29457 cochlilobu
40	771	45.0	330	1	G3P2_LEISHA	Q01558 leishmania
41	770.5	44.9	335	1	G3P2_SCHPO	Q43026 schizosach
42	770.5	44.9	337	1	G3P_CURLU	P28844 curvularia
43	768.5	44.8	336	1	G3P2_ASPMG	Q12552 aspergillus
44	766.5	44.7	336	1	G3P_EMENT	P20445 emeritella
45	762.5	44.5	338	1	G3P_NEUCR	P54118 neurospora

ALIGNMENTS

RESULT 1
G3P_STREY STANDARD; PRT, 335 AA.
AC P50467;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
DR (plasma-binding protein) (Plasma receptor).
GN GAP OR PLR OR GAPA OR SPY0274 OR SPY18_0261.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobactiales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 16103;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-73; 160-173 AND 186-216.
RC STRAIN=64/14;
RX MEDLINE=9235491; PubMed=1322883;
RA Lotenberg R., Broder C.C., Boyle M.D., Kain S.J., Schroeder B.L.,
RA Curtiss R. III;
RT "Cloning, sequence analysis, and expression in Escherichia coli of a
RT streptococcal plasma receptor."
RL J. Bacteriol. 174:5204-5210(1992).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=1196296;
RA Ferretti J.J., Moshan M.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar P.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Koe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus
RT pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbhan K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklets S.M., Porcella S.F.,
RA Pakkine L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Yeary L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
[4]
RP SEQUENCE OF 1-11; 20-30; 103-128; 162-171 AND 199-215.
RC STRAIN=DNS4 / Serotype M6;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins."
RL Submitted (MAY-2000) to Swiss-Prot.
-!- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN.


```

CC -1- CATALYTIC ACTIVITY: D-glycerinaldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M35569; AAA26953.1; -.
DR EMBL: AE006494; AKK3348.1; -.
DR EMBL: AE009973; AAL97041.1; -.
DR HSSP: P00362; 1GDI.
DR InterPro: IPR001173; GAP_dhdtrogenase.
DR InterPro: IPR006424; GAPDH-1.
DR Pfam: PF00044; gpdh; 1.
DR PRINTS: PR00078; G3PDHDEGNASE.
DR TIGRFS: TIGR01534; GAPDH-1; 1.
DR PROSITE: PS00071; GAPDH; 1.
DR GlycoLysis: Oxidoreductase; NAD; Complete proteome.
FT INIT MET 0
FT BINDING 151 151 GLYCERALDEHYDE 3-PHOSPHATE (BY
FT ACT_SITE 178 178 SIMILARITY).
FT ACT_SITE 178 178 ACTIVATES THIOL GROUP DURING CATALYSIS
FT CONFLICT 261 261 (BY SIMILARITY).
FT FT A -> S (IN REF. 1).
SQ SEQUENCE 335 AA; 35811 MW; F0603EE253C8A3F CRC64;
Query Match 99.7%; Score 1709; DB 1; Length 335;
Best Local Similarity 99.7%; Pred. No. 3,4e-111;
Matches 334; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VVKVGNFGRIIGRIAPRIQVNEGVETRIINDLTPNNLAHLKYDTGGPFGTVEVK 61
DB 1 VVKVGNFGRIIGRIAPRIQVNEGVETRIINDLTPNNLAHLKYDTGGPFGTVEVK 60
QY 62 EGGFEVNGFIKXSAERDENIDMTDGEIVLEATGFPKKEAAKHLHANGAKKVVIT 121
DB 61 EGGFEVNGFIKXSAERDENIDMTDGEIVLEATGFPKKEAAKHLHANGAKKVVIT 120
QY 122 AFGNDVKTVEENTNDIIDGTEIVTSGASCTTNCIAPAAALHDAPGICKGLMTTHAY 181
DB 121 AFGNDVKTVEENTNDIIDGTEIVTSGASCTTNCIAPAAALHDAPGICKGLMTTHAY 180
QY 182 TGDQIILDGPHRGCDLRRAAGANIVNSTGAAGAIGLVIPELNGLDGAORVPVPLG 241
DB 181 TGDQIILDGPHRGCDLRRAAGANIVNSTGAAGAIGLVIPELNGLDGAORVPVPLG 240
QY 242 SYTELAVTLDKNSVSEVINAAMKAASNDSEGTEDPIVSSDIWVSYSGLDFDARTKWE 301
DB 241 SYTELAVTLDKNSVSEVINAAMKAASNDSEGTEDPIVSSDIWVSYSGLDFDARTKWE 300
QY 302 VDSQLVKVSVMNEMSTALQVLTLEYFAKIAK 336
DB 301 VDSQLVKVSVMNEMSTALQVLTLEYFAKIAK 335
ID GAP STRS3 STANDARD; PRT; 335 AA.
GAP STRS3
AC Q8K8M9;
DT 28-FEB-2003 (rel. 41, Created);
DT 28-FEB-2003 (rel. 41, Last sequence update);
DE 15-MAR-2004 (rel. 43, Last annotation update);
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)

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DE (Plasminogen-binding protein) (plasmin receptor).
GN GAP OR PLR OR SPY3_0201 OR SPS0207.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M3S315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Bares S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution."
RL Genome Res. 13:1042-1055(2003).
CC -1- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN (By similarity).
CC -1- CATALYTIC ACTIVITY: D-glycerinaldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.
CC -----
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CC -----
DR EMBL: AE014140; AAM78809.1; -.
DR EMBL: AP005141; BAC63302.1; -.
DR InterPro: IPR000173; GAP_dhdtrogenase.
DR InterPro: IPR006424; GAPDH-1.
DR Pfam: PF00044; gpdh; 1.
DR Pfam: PF02800; gpdh; 1.
DR PRINTS: PR00078; G3PDHDEGNASE.
DR TIGRFS: TIGR01534; GAPDH-1; 1.
DR PROSITE: PS00071; GAPDH; 1.
DR GlycoLysis: Oxidoreductase; NAD; Complete proteome.
FT INIT MET 0
FT BINDING 151 151 GLYCERALDEHYDE 3-PHOSPHATE (BY
FT ACT_SITE 178 178 SIMILARITY).
FT ACT_SITE 178 178 ACTIVATES THIOL GROUP DURING CATALYSIS
FT FT (BY SIMILARITY).
SQ SEQUENCE 335 AA; 35841 MW; 4DCB76F382F65698 CRC64;
Query Match 99.4%; Score 1705; DB 1; Length 335;
Best Local Similarity 99.4%; Pred. No. 6,3e-111;
Matches 333; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 VVKVGNFGRIIGRIAPRIQVNEGVETRIINDLTPNNLAHLKYDTGGPFGTVEVK 61
DB 1 VVKVGNFGRIIGRIAPRIQVNEGVETRIINDLTPNNLAHLKYDTGGPFGTVEVK 60
QY 62 EGGFEVNGFIKXSAERDENIDMTDGEIVLEATGFPKKEAAKHLHANGAKKVVIT 121

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Db 61 EGSEVNVNFIKVSARDPENIDWATDGEIVLEATGFPKAEAEKHLHTNGAKKVVIT 120
 QY 122 APGNDVKTIVVFNTHDIIIDGTETVYISGASCTTNCLAPAKALHARSGIKG:MTTHAY 181
 Db 121 ABGNDVKTIVVFNTHDIIIDGTETVYISGASCTTNCLAPAKALHARSGIKG:MTTHAY 180
 QY 182 TGDQMLIDGPHRGDGLRRARAGANIVPNSGAAKALGVIPELNGKLDGAQRVPVPTG 241
 Db 181 TGDQMLIDGPHRGDGLRRARAGANIVPNSGAAKALGVIPELNGKLDGAQRVPVPTG 240
 QY 242 SVTELVTITLDKNVSVDEINAMKAASNSFGYTEDPVSSDIVGVSGLFPATQTKWE 301
 Db 241 SVTELVTITLDKNVSVDEINAMKAASNSFGYTEDPVSSDIVGVSGLFPATQTKWE 300
 QY 302 VDSGLVKVSWYDNEMSYTAQLVRLTEYFAKIAK 336
 Db 301 VDSGLVKVSWYDNEMSYTAQLVRLTEYFAKIAK 335

RESULT 3

G3P_STREQ
 ID G3P_STREQ STANDARD; PRT: 335 AA.
 AC CS9306;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
 DB (Plasminogen-binding protein) (Plasmin receptor).
 GN GAP OR GAPC.
 OS Streptococcus equisimilis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 *OC Streptococcus.
 OX NCBI_TaxID=119602;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H46A;
 RA MEDLINE=96305364; PubMed=8706717;
 RA Gase K., Gase A., Schirmer H., Malke H.;
 RT "Cloning, sequencing and functional overexpression of the
 RT Streptococcus equisimilis H46A gapc gene encoding a
 RT glyceraldehyde-3-phosphate dehydrogenase that also functions as a
 RT plasminogen-binding protein. Purification and biochemical
 RT characterization of the protein.";
 RL Eur. J. Biochem. 239:42-51(1996).
 CC -1- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN.
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: Homotetramer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC
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 CC
 CC EMBL: X57788; CAA66377.1; -
 CC EMBL: Y12602; CAA73174.1; -
 CC PIR: S71350; S71350.
 CC HSSP: P00362; 1GDI.
 CC InterPro: IPR000173; GAP dehydrogenase.
 CC InterPro: IPR006424; GAPDH-1.
 CC Pfam: PF00044; gpdh_1.
 CC Pfam: PF02800; gpdh_C_1.
 CC PRINTS: PR00078; G3PDHDEGNASE.
 CC TIGRFAM: TIGR01534; GAPDH-1; 1.
 CC PROSITE: PS00071; GAPDH: 1.
 CC Glycolysis; Oxidoreductase; NAD.

FT INIT MET 0 0 BY SIMILARITY.
 FT BLINDING 151 151 GLYCERALDEHYDE 3-PHOSPHATE (BY
 FT ACT_SITE 178 178 SIMILARITY).
 FT ACT_SITE ACTIVATES THIOL GROUP DURING CATALYSIS
 SQ SEQUENCE 335 AA; 35739 MW; FE7ACFPED7663B46 CRC64;
 Query Match 94.0%; Score 1612; DB 1; Length 335;
 Best Local Similarity 95.5%; Freq. No. 1.7e-104;
 Matches 320; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

RESULT 4

G3P_LACIA
 ID G3P_LACIA STANDARD; PRT: 337 AA.
 AC P52587;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
 GN GAP OR LD0559.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LM0230;
 RA MEDLINE=95291425; PubMed=7773380;
 RA Cancelli M.R., Hillier A.D., Davidson B.E.;
 RT "Lactococcus lactis glyceraldehyde-3-phosphate dehydrogenase gene,
 RT gap: further evidence for strongly biased codon usage in glycolytic
 RT pathway genes.";
 RL Microbiology 141:1027-1036(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=IL1403;
 CC MEDLINE=21235186; PubMed=11337471;
 CC Bolotin A., Wincker P., Manger S., Jaillon O., Malarre K.,
 CC Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: Homotetramer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.

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DR EMBL: I36307; AAC1453.1; -
DR EMBL: AE006290; AAK04657.1; -
DR PIR: G86694; G86694.
DR HSSP: P17721; IHG.
DR InterPro: IPR00173; GAP dhdtrogenase.
DR InterPro: IPR006424; GAPDH-1.
DR Pfam: PF000044; spdh.1.
DR Pfam: PF02800; spdh.C.1.
DR PRINTS: PR00078; G3PDHGNASE.
DR TIGRFAMs: TIGR01534; GAPDH-1; 1.
DR PROSITE: PS00071; GAPDH; FALSE NEG.
KW Glycolysis; Oxidoreductase; NAD; Complete proteome.
FT BINDING 152 152 GLYCERALDEHYDE 3-PHOSPHATE
FT ACT SITE 179 179 (BY SIMILARITY).
FT CONFLICT 143 143 ACTIVATES THIOL GROUP DURING CATALYSIS
FT SEQUENCE 337 AA; 36057 MW; 17BB8C6AEEF569D CRC64;
SQ
Query Match 78.0%; Score 1338.5; DB 1; Length 337;
Best Local Similarity 77.2%; Pred. No. 1.4e-85;
Matches 260; Conservative 31; Mismatches 45; Indels 1; Gaps 1;

QY 1 MVRKVGINGEGRIGRLAFRIQNEGVETRIINDLTDPMALHLKYDTQGRFGTVEV 60
DB 1 MVRKVGINGEGRIGRLAFRIQNEGVETRIINDLTDPMALHLKYDTQGRFGTVEV 60
QY 61 KEGEYVNGNFIKVAERDENIDMADVEIVLZATGFPKKEAAEKHIANAKKVV 120
DB 61 KEGEYVNGNFIKVAERDENIDMADVEIVLZATGFPKKEAAEKHIANAKKVV 120
QY 121 TAPGNDVKTVPNTNHDITDTEVTSAGSCTTNCLAPMAKALHAFIQGLMTTHA 180
DB 121 TAPGNDVKTVPNTNHDITDTEVTSAGSCTTNCLAPMAKALHAFIQGLMTTHA 180
QY 181 YTGQMTLDGPHRGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAAGVPT 240
DB 181 YTGQMTLDGPHRGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAAGVPT 240
QY 241 GSITELVTLTKNVSVDENINAAKASNDSPGYTDEPIVSSDIVGYSGLFDATQTKM 300
DB 241 GSITELVTLTKNVSVDENINAAKASNDSPGYTDEPIVSSDIVGYSGLFDATQTKM 300
QY 301 EY-DGSQLVKTVMYDNEKSYTAQVLTLEFPKIAK 336
DB 301 EY-DGSQLVKTVMYDNEKSYTAQVLTLEFPKIAK 336
DB 301 DKGQGLVKTVMYDNEKSYTAQVLTLEFPKIAK 337

RESULT 5
G3P_CLOAB STANDARD; PRT; 334 AA.
AC Q59309;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) (CP
DE 17/CP 18).
GN GAP.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RX [1]
RP SEQUENCE FROM N.A.

RA Oster T., Assochei O., Scherrer S., Branlant G., Branlant C.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PARTIAL SEQUENCE OF 1-26.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5";
RL Electrophoresis 15:802-806(1998).
CC -1 CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1 PATHWAY: Second phase of glycolysis; first step.
CC -1 SUBUNIT: Homotrimer (by similarity).
CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
CC -1 SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
CC dehydrogenase family.

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DR EMBL: X72219; CA451020.1; -
DR PIR: S34254; S34254.
DR HSSP: P00362; IGD1.
DR InterPro: IPR00173; GAP dhdtrogenase.
DR InterPro: IPR006424; GAPDH-1.
DR Pfam: PF000044; spdh.1.
DR Pfam: PF02800; spdh.C.1.
DR PRINTS: PR00078; G3PDHGNASE.
DR TIGRFAMs: TIGR01534; GAPDH-1; 1.
DR PROSITE: PS00071; GAPDH; 1.
KW Glycolysis; Oxidoreductase; NAD.
FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
FT ACT SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
SQ SEQUENCE 334 AA; 36078 MW; D1590SD0DA76227 CRC64;
SQ
Query Match 75.2%; Score 1289.5; DB 1; Length 334;
Best Local Similarity 74.3%; Pred. No. 3.4e-82;
Matches 249; Conservative 33; Mismatches 52; Indels 1; Gaps 1;

QY 2 VVRKVGINGEGRIGRLAFRIQNEGVETRIINDLTDPMALHLKYDTQGRFGTVEV 61
DB 2 VVRKVGINGEGRIGRLAFRIQNEGVETRIINDLTDPMALHLKYDTQGRFGTVEV 61
QY 61 KEGEYVNGNFIKVAERDENIDMADVEIVLZATGFPKKEAAEKHIANAKKVV 121
DB 61 KEGEYVNGNFIKVAERDENIDMADVEIVLZATGFPKKEAAEKHIANAKKVV 121
QY 121 TAPGNDVKTVPNTNHDITDTEVTSAGSCTTNCLAPMAKALHAFIQGLMTTHA 181
DB 121 TAPGNDVKTVPNTNHDITDTEVTSAGSCTTNCLAPMAKALHAFIQGLMTTHA 181
QY 181 YTGQMTLDGPHRGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAAGVPT 241
DB 181 YTGQMTLDGPHRGDLRRARAGANIVPNSGAKAIGLVIPELNGKLDGAAGVPT 241
QY 241 GSITELVTLTKNVSVDENINAAKASNDSPGYTDEPIVSSDIVGYSGLFDATQTKM 301
DB 241 GSITELVTLTKNVSVDENINAAKASNDSPGYTDEPIVSSDIVGYSGLFDATQTKM 301
QY 301 EY-DGSQLVKTVMYDNEKSYTAQVLTLEFPKIAK 336
DB 301 EY-DGSQLVKTVMYDNEKSYTAQVLTLEFPKIAK 336
DB 300 VDSQGLVKTVMYDNEKSYTAQVLTLEFPKIAK 334

RESULT 6
G3P_CLOAB STANDARD; PRT; 334 AA.
AC Q59309;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) (CP
DE 17/CP 18).
GN GAP.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RX [1]
RP SEQUENCE FROM N.A.

AC 052631;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase [EC 1.2.1.12] (GAPDH).
 GN GAP OR GAPC OR GAC0709.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxId=1498;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=99392446; PubMed=10463150;
 RA Schreiber W., Durie P.;
 RA "The glyceraldehyde-3-phosphate dehydrogenase of Clostridium
 RT acetobutylicum: isolation and purification of the enzyme, and
 RT sequencing and localization of the gap gene within a cluster of other
 RT glycolytic genes.";
 RL Microbiology 145:1839-1847(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.W., Dubois J., Qiu D., Hittl J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RA "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis, first step.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
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 CC -----
 DR EMBL: AR043386; AAC13160.1; -;
 DR EMBL: AE007586; AAK78686.1; -;
 DR PIR: C96987; C96987.
 DR HSSP: P17721; 1HDG.
 DR InterPro: IPR000173; GAP_dhdrogenase.
 DR InterPro: IPR006424; GAPDH-I.
 DR Pfam: PF00044; spdh.1.
 DR Pfam: PF02800; spdh.C.1.
 DR PRINTS: PRO0078; G3PDHDSGNASE.
 DR TIGRFAMs: TIGR01534; GAPDH-I.1.
 DR PROSITE: PS00071; GAPDH.1.
 DR GlycoLyis: Oxidoreductase; NAD: Complete proteome.
 FT ACT_SITE 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 FT BINDING 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 SQ SEQUENCE 334 AA; 35850 MW; 10552A174BE789B5 CRC64;
 Query Match 73.4%; Score 1259.5; DB 1; Length 334;
 Best Local Similarity 71.9%; Pred. No. 4e-80;
 Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1;
 QY 2 VVKGINGFGRIQLAFRIQNVGCVTRINDLPNNLAHLKYDTGGRFGDGVVVK 61
 DB 1 MAKIINGFGRIQLAFRIQNVGCVTRINDLPNNLAHLKYDTGGRFGDGVVVK 60
 QY 62 EGGEVNGNFIKVSARDPENIDWATGIVIVLAFGPAKKEAAEHLAAMAKKVVIT 121

DB 61 BGAFVNGKEVFAEADPEKLPNGDLIDVLECTGFEFTKEKAEANVA-GAKKVIIS 119
 QY 122 AGGNDKVTVPENVNDHLDGETVIVSGSCCTNCLIAAMAKALDARGIOKIMTTIHAY 181
 DB 120 APAGNDKVTVPENVNDHLDGETVIVSGSCCTNCLIAAMAKALDARGIOKIMTTIHAF 179
 QY 182 TGDQMIIDGPHRQZDLRPARAGANIVPNSGAAGAIGLVIPEINGKLGGAAQRPVPTG 241
 DB 180 TNDQNTIDGPHRQZDLRPARAGANIVPNSGAAGAIGLVIPEINGKLGGAAQRPVPTG 239
 QY 242 SYTELVTTLKRVSYDEINAAKASNDGFTEDPIVSDIVGVSYSLFPAOTKXME 301
 DB 240 SITEVLVLLKKKVTVEEINAAKASNDGFTEDPIVSDIVGVSYSLFPAOTKXIVD 299
 QY 302 VDSGLVKVSWTDNBSYTAQVLETFEFAIKAK 336
 DB 300 VNSQLVKTAWIDWMSYTSQVRLTAIFAKIAK 334
 RESULT 7
 GAPL STRAP STANDARD; PRT; 336 AA.
 ID GAPL STRAP STANDARD; PRT; 336 AA.
 AC Q8CFY5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12) (GAPDH 1).
 GN GAPC OR GAP OR SE0557.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RX PubMed=12850922;
 RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
 RA Qin Z.-Q., Mao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
 RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
 RA "Genome-based analysis of virulence genes in a non-biofilm-forming
 RT Staphylococcus epidermidis strain (ATCC 12228)."
 RL Mol. Microbiol. 49:1577-1593(2003).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis, first step.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE016745; AA004154.1; -;
 DR InterPro: IPR006424; GAP_dhdrogenase.
 DR InterPro: IPR000173; GAP_dhdrogenase.
 DR Pfam: PF00044; spdh.1.
 DR Pfam: PF02800; spdh.C.1.
 DR PRINTS: PRO0078; G3PDHDSGNASE.
 DR TIGRFAMs: TIGR01534; GAPDH-I.1.
 DR PROSITE: PS00071; GAPDH.1.
 DR GlycoLyis: Oxidoreductase; NAD: Complete proteome.
 FT BINDING 151 151 GLYCERALDEHYDE 3-PHOSPHATE.
 FT ACT_SITE 178 178 SIMILARITY.
 FT ACTIVATES THIOL GROUP DURING CATALYSIS.
 SQ SEQUENCE 336 AA; 36190 MW; A96220202A5767 CRC64;
 Query Match 69.4%; Score 1190; DB 1; Length 336;

Best Local Similarity 69.4%; Pred. No. 2,6e-75;
Matches 224; Conservative 39; Mismatches 62; Indels 2; Gaps 2;

QY 1 MAVKVGINGFGRIGRLARRIIONVEVETRIINDLTPNMLAHLYKTTTQREGEVEV 60
DB 1 MAIKVAINSGRIGRLAFRRIQDVEGLVAVVNDLDDMLAHLYKTTTQREGEVEV 60
QY 61 KXGFEVNGFIVKSAERDPENIDMAIDGVEIYLAATGFPKXKAERKHLNAGKAKVI 120
DB 61 TGGFRVNGKEIKSFEPDAGKLPMGDLIDVLECTGFYTKKQAHIDA-GAKKVL 119
QY 121 TAPGNDVKTVENINHDLDGTEVIGSACTTNCAPMAKALHDAFGIOKGLMTTIIH 180
DB 120 SAPAGGVKTIVENTHTLDOSSEIVSASCTTNSAPVAKVLSEDFGLVEGFWTTIIH 179
QY 181 YTGDMILDPHGGRLRRARAGAAIVPNSGAKAGLVPELNGKIDGAGGVPPV 240
DB 180 YTGDMITQDAPHRKGGKRRARAAENITPNSGAKAGLVPELNGKIDGAGGVPPV 239
QY 241 GSVELEVVTLDK-NVSVEINAAKMAKASNDSEFGYTEPIVSDIVSVSGSLFDATCTKV 239
DB 240 GSVELEVVTLDKQDVTYVQVANSKAKSDSEFGYTEPIVSDIVSVSGSLFDATCTKV 239
QY 300 MEVDGSQLVYVSWYDNEMSYTAQVLTLEFPAKJAK 336
DB 300 MIVGDRQVYVAAVYDNEMSYTAQVLTLEFPAKJAK 336

RESULT 8
G3P1 STAM STANDARD; PRT; 336 AA.
ID 15-MAR-2004 (Rel. 43, Last sequence update)
AC 0925C5;
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DB Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12) (GAPDH 1).
GN GAPA OR GAP2 OR SAV0772 OR SA0727 OR MW0734.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OS Staphylococcus aureus (strain N315).
OS Staphylococcus aureus (strain MW2), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBI_TaxID=15878, 158879, 196620, 1280;
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DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
 GN GAP.
 OS Lactobacillus delbrueckii (subsp. bulgaricus).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 OX NCBI_TaxId=1585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BI07;
 RX MEDLINE=98240227; PubMed=9579064;
 RA Bramy P., Delatorre F., Garel J.R.;
 RT "An operon encoding three glycolytic enzymes in Lactobacillus
 RT delbrueckii subsp. bulgaricus: glyceraldehyde-3-phosphate
 RT dehydrogenase, phosphoglycerate kinase and triosephosphate
 RT isomerase.";
 RL Microbiology 144:905-914(1998).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
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 CC -----
 DR EMBL, AJ000339; CAA04014.1; -
 DR PIR, T09633; T09633.
 DR HSSP, P17721; IHG.
 DR InterPro: IPR000173; GAP dhdrogenase.
 DR InterPro: IPR006424; GAPDH-I.
 DR Pfam: PF00044; gpdh. 1.
 DR Pfam: PF00078; G3PDHGRNAS.
 DR PRINTS: PR00078; G3PDHGRNAS.
 DR TIGRfam: TIGR01534; GAPDH-I; 1.
 DR PROSITE: PS00071; GAPDH; FALSB NEG.
 DR GlycoLysis; NAD; Oxidoreductase.
 FT BINDING 156 156 GLYCERALDEHYDE 3-PHOSPHATE
 FT (BY SIMILARITY).
 FT ACT SITE 183 183 ACTIVATES THIOL GROUP DURING CATALYSIS
 FT (BY SIMILARITY).
 FT SEQUENCE 338 AA; 36564 MW; DF978C9CA4F7DFA CRC64;
 Query Match 58.5%; Score 1003; DB 1; Length 338;
 Best Local Similarity 58.7%; Pred. No. 2,26-62;
 Matches 193; Conservative 45; Mismatches 89; Indels 6; Gaps 3;
 QY 1 MVAKVGINGFGRIGLAARRI---ONVGEVTRINDLTDPMMLAKLTKYDQGFDS 56
 DB 1 MVAKVGINGFGRIGLAARRIMDLSGETMDIEVAINDLTPPMLAKLTKDSTHGPFDR 60
 QY 57 TVEVKGCFEUNGNFIKYSARPEPITMA-TDGEVLYEATGFFAKKAAEKILANNA 115
 DB 61 EVSATSDSLVVGKKYRYVAEPQANIPWKNXDGVDVLECTGFYSYAKAQATLID-CA 119
 QY 116 KXVITAPGNDYKVVVNNHDLILGTEVYSGASCTTGCLAPAKALHAPGIGQKGLM 175
 DB 120 KXVITAPGNDLKTIVSYNQTLLADDTIYSAGSCTTSLAPANALNKEFGIYQGTW 179
 QY 176 TTHAYTGQMLDGPFRGDLRRAPAGANIVPNSGAAKALGIVTELNKLDGAQR 235
 DB 180 TTHAYTATQKVLDCGPRGANNFNAAALANIIPSTGAKAKALGIVTELNKLDGAQR 239
 QY 236 VVPVTSVTEIVTIDKQVSDVDENAKAASNSFGITDPIYSQDIVIGVSYGSLFPA 295
 DB 240 VVPVDSSETELVITIDKKVTAEEVNAAMKRYESBPANADQIVTDVIGTASIDPPI 299

QY 296 OTKWEVDQSOLKVVSWYDNEMSYTAQVLTLEYPAKI 334
 DB 300 QTVQVTAEDKQVLYAVYDNEYSFTQMTILHRAHRL 338
 RESULT 10
 ID GAP3_ECO57 STANDARD; PRT; 333 AA.
 AC P56072;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12) (GAPDH-C).
 GN GAPC OR 22304 OR ECS2022.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxId=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor V., Kirkpatrick N.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobleck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Nantharajan T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 050952;
 RX MEDLINE=21156231; PubMed=11258196.
 RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Yanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:111-22(2001).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
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 CC -----
 DR EMBL, AB005364; AA056359.1; -
 DR EMBL, AF002557; BAB35445.1; -
 DR PIR, C85737; C85737.
 DR PIR, F90881; F90881.
 DR HSSP, P17721; IHG.
 DR InterPro: IPR000173; GAP dhdrogenase.
 DR InterPro: IPR006424; GAPDH-I.
 DR Pfam: PF00044; gpdh. 1.
 DR Pfam: PF02800; gpdh. C; 1.
 DR PRINTS: PR00078; G3PDHGRNAS.
 DR TIGRfam: TIGR01534; GAPDH-I; 1.
 DR PROSITE: PS00071; GAPDH; 1.
 DR GlycoLysis; Oxidoreductase; NAD; Multigene family; Complete proteome.
 FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE
 FT (BY SIMILARITY).


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CC -----
DR EMBL; AE000040; AAB96059.1; -.
DR PIR; S73737; S73737-.
DR HSSP; P17721; LHDS.
DR InterPro; IPR000173; GAP_dhdrogenase-.
DR InterPro; IPR006424; GAPDH-1.
DR Pfam; PF00044; gpdh_c_1.
DR Pfam; PF02800; gpoh_C_1.
DR PRINTS; PRD0078; G3PDHGRASE.
DR TIGRFAMs; TIGR01534; GAPDH-1; 1.
DR PROSITE; PS00071; GAPDH; 1.
KW Glycolysis; Oxidoreductase; NAD; Complete proteome.
FT BINDING 157 157 GLYCERALDEHYDE 3-PHOSPHATE
   (BY SIMILARITY).
FT ACT_SITE 184 184 ACTIVATES THIOL GROUP DURING CATALYSIS
   (BY SIMILARITY).
SQ SEQUENCE 337 AA; 36805 MM; 550747A529ABCA83 CRC64;
Query Match 53.7%; Score 921; DB 1; Length 337;
Best Local Similarity 54.1%; Pred. No. 1e-56;
Matches 180; Conservative 54; Mismatches 95; Indels 4; Gaps 3;
QY 3 VKGNGEFGRIGLAFRRIQNVEGVETRRINDITDPNKMLAKTTOGGKRDGTVEVGE 62
   ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 IRVALNGFERIGRLVFRRALISOKNIEIVANNDIHRDTLAILTKYDSAGFEKKKKVAKD 67
QY 63 GGFEEWKNFIVASERBPENIDMADGVEITELACGFFAKKEAAEKHLIAANKKKVITA 122
   :::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 NTLMATKKVKLVFSSKPDLMAFNHNIDIVSGTRVSSEGSALHQA-QAKRVIIISA 126
QY 123 PG-GNDVKTVPENTHDILDGTEIVYSIGASCCTNCIAPMAPALAHDAFGIOKLMTTHAY 181
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 PAQDKIKTVVVNNHKTIINAEKXIIISASCCTNCIAPMVHLEKPKFGLHGTWTLYHAY 186
QY 182 TGDMILIDGFRGGDIARRAGAANIYNSGTGAARKIGINPELNKGTLGAAGORVPVPTG 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 TADRDLDQDPH-SDLERRAAAACNVETTTGAKRIGVAPPAATGKLGMALRPVLTG 244
QY 242 SVTELAVTLDDKNVSYVDINAMKAASNDSCGYEDPIVSDDIVGVSYSGLFPDATOTKME 301
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 245 SYVELCALALEKNAVTEQIDINMKMKKAASPFYCEDEIVSDIVSEHGSIPLSKLTNIIE 304
QY 302 VDSQLVKTVMSTYDNEMKSTTAQIVTLEYRKTI 334
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 305 VDGNKLYKYVAWYNDESSYNOIYEVVNYCAKL 337
RESULT 13
GAP_CORGL
ID GAP CORGL STANDARD; PRT; 334 AA.
AC Q01651;
DT 01-APR-1993 (Rel. 25, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
GN GAP OR CGJ1588.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
[1]
RN [SEQUENCE FROM N.A.
RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=93015645; PubMed=1400156;
RA Elkmann B.-U.;
RT "Identification, sequence analysis, and expression of a
   Corynebacterium glutamicum gene cluster encoding the three glycolytic
   enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate
   kinase, and triosephosphate isomerase."
KT
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RL J. Bacteriol. 174:6076-6086(1992).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RT Submitted (MAY-2002) to the EMBL/Genbank/DBD databases.
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
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CC EMBL: X59403; CAA42045.1; -;
 CC EMBL: AP005279; BAB98981.1; -;
 CC PIR: A43260; A43260.
 CC HSSP: P00362; 1GDI.
 CC InterPro: IPR003173; GAP dehydrogenase.
 CC InterPro: IPR006424; GAPDH-1.
 CC Pfam: PF00044; spdh; 1.
 CC Pfam: PF02800; spdh C; 1.
 CC PRINTS: PRO0078; 3EDHGNASE.
 CC TIGRFS: TIGR01534; GAPDH-1; 1.
 CC PROSITE: PS00071; GAPDH; 1.
 CC GLYCOLYSIS; Oxidoreductase; NAD; Complete proteome.
 CC BINDING 153 153
 CC ACTIVATES THIOL GROUP DURING CATALYSIS.
 CC ACT SITE 180 180
 CC CONFLICT 25 26 SD -> NG (IN REF. 1).
 CC CONFLICT 333 334 KL -> QALN (IN REF. 1).
 CC SEQUENCE 334 AA; 36045 MW; 33792AF65FA90EF7 CRC64;

Query Match 53.0%; Score 908.5; DB 1; Length 334;
 Best Local Similarity 56.2%; Pred. No. 7.4e-56;
 Matches 150; Conservative 4; Mismatches 94; Indels 13; Gaps 6;

QY 1 MVRKVGNGRIGRLAERLI QNVEGEVTRINDLDPNMLAHLLKNTDQGRPDGVE 59
 DB 1 MTRVINGRFRIGRNFPRVFRERSDLEVAVNDLTKTSTLLNFDISMGDLQZVE 60
 QY 60 VKEGFEVNGNFIKVSAREPENIDATDVEIVLENTGFPAKKEAKELHANGAKV 119
 DB 61 YDDSDITVGGRIAYARERPKULMAAHNDIVIESTGFTDAAAHTEA-GAKVIT 119
 QY 120 ITAPGNDVKTAVNTNHD-LD-GRETVISGASTTNCIAPAKALHARISQKMTTI 178
 DB 120 ISAPASNEDEAFVGVNHSYDEPHNNTISGASCTTNCIAPAKALNKPRIENGMTTV 179
 QY 179 HATGPDMLDGPGRGDLARRAAGANIVNNGAKKAGIVTEINGKIDGAARVY 238
 DB 183 HATGPDRLHDPHR--DLRRAPAAVNIPTSGAKKALVHDELKIDGALRAVY 237
 QY 239 PEGSVTELVVTLDKKVSDEINAKMAKASNDSPG---YTEDPIVSDIVGVSYGIFDA 294
 DB 238 ITGSGATDLTFNFKSEVIVESINAKIKBAVGEFETLAVSEBELVSTDIVHDSGISFDA 297
 QY 295 TQKRVEDGSQLYVVSQYDNEMSTYQALVFTLEFYA 332
 DB 298 GLTKV---SGNTVYVVSQYDNEMGYTCQLRLTELVA 331

RESULT 14
 GAP_MTCGE STANDARD; PCT; 337 AA.
 ID GAP_MTCGE

AC P47543;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
 GN GAPD OR GAP OR MG301.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 CX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96026346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
 RA Nguyen D.T., Uetshack T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bock K.F., Hu P.-C., Luetter T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RT Science 270:397-403(1995).
 RN [2]
 RP SEQUENCE OF 1-81 AND 279-337 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=94075230; PubMed=8253680;
 RA Peterson S.N., Hu P.-C., Bock K.F., Hutchison C.A. III;
 RT "A survey of the Mycoplasma genitalium genome by using random
 RT sequencing.";
 RT J. Bacteriol. 175:7918-7930(1993).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -1- PATHWAY: Second phase of glycolysis; first step.
 CC -1- SUBUNIT: Homotetramer (By similarity).
 CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
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 CC -----

QY 3 VVGVINGRIGRLAERLI QNVEGEVTRINDLDPNMLAHLLKNTDQGRPDGVEYKE 62
 DB 8 IVVAINGRGIRGRLAERLI QNVEGEVTRINDLDPNMLAHLLKNTDQGRPDGVEYKE 67
 Query Match 52.9%; Score 908; DB 1; Length 337;
 Best Local Similarity 53.2%; Pred. No. 8.2e-56;
 Matches 177; Conservative 54; Mismatches 98; Indels 4; Gaps 3;

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QY 63 GGEVNFNFIKVAERDPENIDMATDVEIVLRTATGFAKKEAAMKHLNANGAKKVITA 122
DB 68 NIIQIDREKVVYFSEEDPONTLPMDHDIDVISTRTFVSEGSAMHKA-GAKRITISA 126
QY 123 PG-GNDVATVFNTHDILDTETVTSAGSTTNCIAPAKALHDAFGIOKIMTTIAY 181
DB 127 PAKERTIRTVVYNNHKTISDDKIISAASCTTICLAPVHLLEKNEGIYVGTMLVHAY 186
QY 182 TSDQMTIDGPHRGDULRRARAGANIVNNGAAXKIGVPELNGKIDGAAQRPVPTG 241
DB 187 TMDQRIQDAFH-NDLRRRAAAAVIVPTTGAAKKIGLVEPANGKLNKSLKVPVLTG 244
QY 242 SATETVTLTDKNVSVDEINNAAMKASNDSPGYEDDPIVSSDVGVSFLDATTQKWE 301
DB 245 STYELSTVLEKSPSEVQWQAKRRPASLFCYEDCPVSDVSVSEIGSIFDKLNTIYE 304
QY 302 VDSGQIVKVSWMYDNEMSYTQOLVETLEFPYAKI 334
DB 305 VDSMKLYKVYAMVYDNEMSYVHQLVAVVSYCAKL 337

RESULT 15
G3P1_BACSU STANDARD; PRT; 334 AA.
ID 01-MAR-1989 (Rel. 10, Created)
AC P09124;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12) (GAPDH) (NMD-
  dependent glyceraldehyde 3-phosphate dehydrogenase).
GN GABA OR GAP OR B5133940.
CS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CC NCBI TaxID=1423;
CX [1]
RX SEQUENCE FROM N.A.
RC STRAIN=168 / BD170;
RX MEDLINE=89160255; PubMed=2493623;
RA Viene A., Dhase P.;
RT "Sequence of the glyceraldehyde-3-phosphate dehydrogenase gene from
  Bacillus subtilis.";
RL Nucleic Acids Res. 17:1251-1251(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=86044033; PubMed=3384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
  Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcher S.,
  Boriss R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
  Broillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
  Choi S.K., Codani J.J., Comerion I.F., Cummings N.J., Daniel R.A.,
  Denzot F., Devine K.M., Dusterhoft A., Enlich S.D., Emerson P.T.,
  Ertlan K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
  Fritz C.Y., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
  Ghm S.Y., Glaeser P., Goffeau A., Goldlighty E.J., Grandi G.,
  Guisepi G., Guy B.J., Haga K., Halesch J., Harwood C.R., Henaut A.,
  Hilbert H., Holstapel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
  Joris B., Karamata D., Kasahara Y., Kleier-Blanchard M., Klein C.,
  Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
  Kurita K., Lapidus A., Lardinois S., Lander J., Lazarevic V.,
  Lee S.M., Levine A., Liu H., Masuda S., Manel C., Medigue C.,
  Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
  Moore D., O'Reilly M., Ogawa K., Ogizawa A., Oudega B., Park S.H.,
  Parro V., Pohl T.M., Portetelle D., Porollik S., Prescott A.M.,
  Priesen B., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
  Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate I.,
  Sato T., Scanlan E., Schleich S., Schroeder R., Scotfene F.,
  Sekiguchi J., Sekowska A., Serot S.J., Serron P., Shin B.S., Sollo B.,
  Sorokin A., Taccini B., Takagi T., Takahashi H., Takemaru K.,
  Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Toomari A.,
  Tosi V., Uchiyama S., Vandebol M., Vannier F., Vassartti A.,
  Viatto A., Wambutt R., Wedler E., Wedler H., Weitznagel T.,
  Winters P., Wipat A., Yamamoto S., Yamane K., Yasumoto K., Yata K.,

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RA Yoshida K., Yoshikawa H.F., Zimstein E., Yoshikawa H., Darchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
  subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-30.
RC STRAIN=168 / JH642;
RX MEDLINE=96345623; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20261518; PubMed=10799476;
RA Fillingner S., Bockel-Muller S., Azza S., Deryn E., Brantant G.,
  Americh S.;
RT "Two glyceraldehyde-3-phosphate dehydrogenases with opposite
  physiological roles in a nonphotosynthetic bacterium.";
RL J. Biol. Chem. 275:14031-14037(2000).
CC -1- FUNCTION: More active in catabolism.
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
  NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
  dehydrogenase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
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  or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: X13011; CAJ31434.1; -
DR EMBL: Z99121; CAB15399.1; -
DR PIR: S02754; DEBSG.
DR HSP: P00362; IGDI.
DR Subtilist; BGI0827; gppA.
DR Interpro; IPR000173; GAP_dhrogenase.
DR Interpro; IPR006424; GAPDH-1.
DR Pfam; PF00044; gpdh_1.
DR Pfam; PF02800; gpdh_C_1.
DR PRINTS; PR00078; G3PDHRCNASE.
DR TIGRPFAM; TIGR01534; GAPDH-1; 1.
DR PROSITE; PS00071; GAPDH.
KM Glycolysis; Oxidoreductase; NAD; Multigene family; Complete proteome.
FT INIT MET 0
FT BINDING 151 151 GLYCERALDEHYDE 3-PHOSPHATE.
FT ACT SITE 178 178 ACTIVATES THIOL GROUP DURING CATALYSIS.
SQ SEQUENCE 334 AA; 35701 MW; 1283D3B6CF5095EC CRC64;

Query Match 52.0%; Score 891.5; DB 1; Length 334;
Best Local Similarity 54.5%; Pred. No. 1.1e-54;
Matches 103; Conservative 41; Mismatch 101; Indels 11; Gaps 5;

QY 3 VVVGINGFGHIGLAFRRIGVGEVTRINDITPNMIALHLYKDTTQGRFGDVEYKE 62
DB 2 VVVGINGFGHIGVNRVRAALNNPEVAVVNDITANLALHLYGDSVHCKLDAEVSVDG 61
QY 63 GGEVNFNFIKVAERDPENIDMATDVEIVLRTATGFAKKEAAMKHLNANGAKKVITA 122
DB 62 NNLVYNGKTEVSAERDPKLSMKQCEVIVVSTGFTKADAKKLEA-GAKRITISA 120
QY 123 PGNDVATVFNTHDILDTETVTSAGSTTNCIAPAKALHDAFGIOKIMTTIAY 181
DB 121 PAKERTIRTVVYNNHKTISDDKIISAASCTTICLAPVHLLEKNEGIYVGTMLVHAY 180
QY 182 TSDQMTIDGPHRGDULRRARAGANIVNNGAAXKIGVPELNGKIDGAAQRPVPTG 241
DB 181 TMDQRIQDAFH-NDLRRRAAAAVIVPTTGAAKKIGLVEPANGKLNKSLKVPVLTG 238

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Thu May 6 08:16:12 2004

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